

501/586

&lt;210&gt; 784

&lt;211&gt; 537

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC006073.

&lt;400&gt; 784

ttaatttttg acttaaactt accaatatta catttccttt tcagactgag aaataactta 60  
attcgattaa atgcgacttt attaatggaa actataattt atcagagggc gcacattttt 120  
atcgcaactta ccacccaatg aatcaaaaac tcggggctgt ctctttctac cgaaaacttt 180  
tggccaagaa agcgctggca attctgcaat tcaattgggc ggccgtccgt ctttctttct 240  
tctcgggctc tctgcagtct tcacettgcc actttgcccg gttggaaaag taaacacaat 300  
ctgattgtat ggcttagata atagccccct tgtgcgccag tgtgtgtgtg tgtgtgtgtg 360  
tctgtgagtg tgttggccag ttggaggagg atggggctaa aaaaaaacga gtgagaaacc 420  
accgacgcgc tgcattgcaac atgttcgccg tcgaacgtca aacgacgagc atcgaacgtc 480  
gaacttcgaa catcgaacgt ggagccgacg aagagtgcgt cggattttac ttaccgc 537

&lt;210&gt; 785

&lt;211&gt; 720

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(720)

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&lt;223&gt; Area matching Drosophila Genomic sequence

AC004299. Matches in area of ORF with sequence  
similarity to Human C-TAK1 gene.

&lt;400&gt; 785

gctgagcttg tgcaacagca gtagaaatag gagagagcaa ttagagaga gaccgaaaac 60  
aaacacacgc acaagagctc acctccacca caggtgtgta ggtgccactt cgtttttctc 120  
tctcgcgcac tctcttttgc tatgtatgta attgtgtggt taggtatatt gccctccctt 180  
tcacatcccc acatcgcttg ccgtgtgttt atttcagtgt caccggggag acagattagc 240  
tcttgctcgc ctgttgctgt aaatatcacg cacacacgct tcccgctcgc ccatctgtac 300  
atacatatgt acatacgtag aaatggaagt tgctagctgt gtgtttaatt cattttcgag 360  
gttttaaatgc gcaacaactg cgacttggtg tgtgttggtt agacgacaaa aaacaaacaa 420  
aagtaacggt gagaatttag aaagcccaat gcaaacgaac gcacacacaa gcacttactc 480  
ctgtcgggtg gagctgcatt gtacttccga agccccaaga ccaatttaat aattttcccc 540  
aaactcacag tgtaagaaca ataaacacgc caagcgcact tgaaaaagaa ataagaaaaa 600  
agaaaaagtt ggcactttcg agcacaagta cttggcacca cacactcagg gaagagtgcc 660  
acgacaaaaa aatttagaga aaaaaccgga aaaccgaatc acacaaacgg aggactatgg 720

&lt;210&gt; 786

&lt;211&gt; 599

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(599)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004115.

&lt;400&gt; 786

ggcagaccgg taagtaagcc aaatactccg gaataaagtt atagcctccg atctctaact 60

tccagcctga gactgcacga tgggtgcctg agggacgttg agcagcaaca acggcgcaaa 120  
cacgagaata cctacacgct gcagcagcaa atagacatga ccaagcaact gaaagccagg 180  
gaggcgtcta gcaactcctc tgacacgccc gtacctccat cgacgcacg cgacacagagt 240  
aatcttcaag cggagaagcc agcagtgcaa aatgaaggcg aggctttcag aggtgttcct 300  
caggggtggaa cgactaatca cgatggaagc ccgccaactg acatagcttg atcacaaata 360  
tgcccctaaa tatgcaccta ttaaaatcta agactaagtc ggggaaaaca agaatttcgt 420  
tgtttcaaatg tacgcatttt tgaagatttt aagatttcgt cttaagaaca gttgacagca 480  
tctttacgct ggttggatcg ttttcaagtt ggtgaagcct tttgcgcacg ggaatataat 540  
taaacaacgt ggtaagaatc aatcttacca agcgaaataa gactgcaggc taacaaggg 599

<210> 787

<211> 581

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(581)

<223> Area matching *Drosophila* Genomic sequence

AC004716.

<400> 787

ggcgaaggta aacgcgaagg cttccgaggc acgtaaaaaa aaagttcaaa cccgactagg 60  
acaacaacgc gaacaggaca ctacacgcga ggcaatcagc cgacacgcga cacagtcacg 120  
agtcggaaaa gcttgtaagg accacaattc gccgcactcc gaatgtgtgt taaagcttcg 180  
tgaaatcctg gggaaataat atcccgcaaa tatccttgca gcgcaatgtg aaagggaatg 240  
ggcattcata aatttataaa tttaaaaaaa aatcataata aaattagaaa aaatattttt 300  
atttataccc aactgcccta aaagtataat ttttgtatat cttaattttt aaatatttat 360  
atttggettta gataatattt tcaaaaaaatt aagagactta ttaccaattt tcatactatt 420  
tggtcttgca tattctttcc ctgctttaag tagaaagcag tctgcactgc ttttagttt 480

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aagtagaatg atatatTTTT tcatagacca taagcaaaaa atcttttagc tgctaaatga 540  
atctacgtgt ggtaatgctc ctcttctcag ttcaaaccaa a 581

&lt;210&gt; 788

&lt;211&gt; 628

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(628)

<223> Area matching *Drosophila* Genomic sequence

AC005889.

&lt;400&gt; 788

caccaacgat tggctagttg ggagggggcg gtggatgtct aacattgcaa cgtgaccatc 60  
gcgcattgcc tttgcacttg taacatgttg ttggagtcgc gtttttttcg ttagcccggg 120  
ttttgttggc tttgttgctg ctgtaaactt gttcgcgttg catgccaatg aggcgcatc 180  
gacgtcaggc ggatttggtg acacagaaac tggattagag gcaacaacca atcaaccaa 240  
tgagtgaaaa aaaaaacaac ttggaaccca aaactagaca ctaagccatg aaaattgtgg 300  
gaaactaagt atttacttta tgattcaata attatacctc ttaaataaac tggttttggc 360  
aacgtaaaaa aatttggttt cacacaaatt gtaatttggtg tacggtactt ttgaagcaaa 420  
gcaaaaattg ttcttttaggt atatcttttt tctatttact aataaaataa ataaataact 480  
ttaaaaaaaaa atttgtgtgc taaaacccaa atatttactt attattatgg gtatgtaaat 540  
ttggtcagca cctgcccact gtgcgcacgt catcggttgc atgccttggtg gttggtgggtg 600  
cttctgcttt ggggggtttct tgggtttt 628

&lt;210&gt; 789

&lt;211&gt; 536

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(536)

<223> Area matching Drosophila Genomic sequence L4908.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation  
factor.

<400> 789

```
ccccacagat acggtgagag aacgacaaga gagagagagg gagcgagagc agctgtgcga 60
tgccggcaga ccaatgttgt tgttattggt gttgtttggc ttggccatct tttagttggt 120
attattgctt tttagtagtg acctccgaca acaaaccgaa atcgaaacaa gttttaagca 180
acaacaacaa cagaaaaaaaa aagaactgca ttaaagcaga gatttatggt tctttaatca 240
aagtctgaag aatgcaaagg cattcctttg ccatgagtat tgcatttgta aaaaaggaaa 300
ctgaaaaaat ttgggattta tgtttttctt tttttgtcta acaaattttg tgctattata 360
atggaaatgt taatgatatt tgtggctctt ggggaaaatg ttttatatca attcatttca 420
cctgggtatc tacttgccgt agaaatcaaa tgcaataaaa aattacagtc aagatttagc 480
caattgttgc gtattttgag ccatttgtgc ttttagacac eggcttggtt gaattc 536
```

<210> 790

<211> 86

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> Complement((1)..(86))

<223> Area matching Drosophila Genomic sequence. Matches  
in area of ORF with sequence similarity to a mouse

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G protein.

&lt;400&gt; 790

ctatagtcgc tctagctccg ttctccgaag agagagagtg aacgaagaga ggcgaggaag 60  
agagttccag gaaatcgcaa gaattc 86

&lt;210&gt; 791

&lt;211&gt; 573

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(537))

<223> Area matching *Drosophila* Genomic sequence

AC004306.

&lt;400&gt; 791

ggcgcaactt gttttcgatg ttgttggtgt cgttgctgct ggcttacgtt ttttttatg 60  
cgccgctcgg gttggtaatg atcttcgtgc atgtgggttg gcgtcggtgt tgtttttggt 120  
gctggtgatg tcggtggatg tagagaagga tgaggaggtg actgcgactg ttgcgttcat 180  
tagcggggca gaggtttttt tgggtttggt gtatggtata tggccagaag gagggcgtgc 240  
gatacatggt ccaggtagac acatgacgaa gccacagtcg aactcccata acccgtcatt 300  
ttactaattg aatacatttg tagtgaaaac gaacccttcg attcggtttt aaaatcattt 360  
tttagagatt taattttgat ttttcagtta aactttgcac ataactgata agtgtacggt 420  
tcatactttc ggagtttcac tgtatttata aacaaattca cccacatggc agcctcgatt 480  
gggtggcggc atatcccgcc gatttcggcg tgggctgatt ttagccgcat tcgatttcca 540  
tttcgggttc aagacttgcc cttcaacttt ggt 573

&lt;210&gt; 792

&lt;211&gt; 648

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&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(648)

<223> Area matching *Drosophila* genomic sequence AC006472

(71606-72257). NPS1077 lies in an intron of a  
gene at 62506-79351bp coding for a 1876AA protein  
similar to hypothetical genes from yeast and  
human.

&lt;400&gt; 792

ctccttacc atgtaacgtt tcgccaacgt gtgcgagcga gagggcgcggt gtgtaatttg 60  
ttgtggagca gctgcgacgg cggggccaaa gctgttgtct cgctcccccg ttcggagtga 120  
ggccttgatt ccggactccg agctccggat caaatatttc aacagttttg gatccgtagg 180  
gagggagggg gatattctagc ctccctagaaa agtttttgcca ttcaaattag tatkataaca 240  
aatacttggc ttagaatggc accatttgcc caacaatccc ctaaaaagta atcgtttgtg 300  
ggacaaacta tgctacagat cccgtttttct tgacagtaaa tggcatattc ctcaaaaatt 360  
aaaaaaaaatg ataaaaaaaa aatgataac aaaacagagt catatacttc agtattttga 420  
aatttctaac aatctatatc tgccatttaa aaagcctgat aagttttcaa gttattcgaa 480  
ctcagtagga ttaccaaatt ttcactgata ttcaatgttg gaatggaagt actaggataa 540  
cccacggaat ttatagtaag aaaaggtcta ggaatttggt ggattcatgg agaaattatc 600  
ggatagaaaa tccttactac ttaacgatag cccaattgag atatagct 648

&lt;210&gt; 793

&lt;211&gt; 463

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

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&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(463))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC006092.

&lt;400&gt; 793

gtctgaggta ttaaatagtg aaaaaaaatg tctgccgcgc cgaaaattga caaagcgacg 60  
ccgccatgtc gcaacctata gccatctccc tctcgcagcg tgctcccagc accaccagtg 120  
ttcatctatg tgtgtagtgc atatttcgag cggttaaaatc tggtgaaaat ttaaaacat 180  
tcaaacagtg gaaaatattg tgcacacatt atagggttttt cacatttccc ttgcggaaat 240  
cggaaaagca agcgtatgtg tgccgaatgg aaaaaaccaa gacgcagggt tgcatttttc 300  
ttgatttcga ggggtgcatt ctgtgtgata agcgtttttt tattctgtct ttaaaatgat 360  
tgtagacttt tgtcccgta tgtttcgata atggatatta cgcagcggca aaattattat 420  
ttaatgtctg ttattgagtc aatgaacttt ctgcgggttg gcc 463

&lt;210&gt; 794

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(519)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC006073.

&lt;400&gt; 794

ggttcgagtt tgaaatgagg tctcaggagc ttcgtgttgc atcgaacctg ctcgatggca 60  
tctattggtg agaggggcgt tctgtgttcg caataaccgg aaacggaaat catatttggt 120  
caagttctaa tgccatcaac gattgcaatt aaatggccaa atgtcaattg tttcaagctg 180



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actaagtgcg agaaggacaa aaaagtgttg tgcgaaaaga gacaggcgcc aaaagcctga 240  
acctgccatt aaccgttaat gcacggatcg taaatcgaat tgaaaggaag ggtgtgtcat 300  
gccggactta taaataaaat taacaaccag ccgggggaaag aggttaaggc ggaaatattt 360  
gcgccactgc gactttcttg ctgcgtcgat tgggtcccgtt gttttttggt gcttgtaatt 420  
aatgggcaaa caattacaaa aaaaaaataa agggagtcgg ggcaagaaga atgaggcccc 480  
cagtgggaatt taccagtatt aaagggcgag aagcaagtt 519

&lt;210&gt; 795

&lt;211&gt; 704

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(704))

<223> Area matching *Drosophila* Genomic sequence

AC007176.

&lt;400&gt; 795

atacaccta tttacgttta ctaagagagc gaccaacgcg agacgagtcc caaaatgagc 60  
gctctttttg ccgaactggt gaatgccggc tgcaaaagca acaatacaac tgcacacatc 120  
accacccccca ttgcgcttat gtttttagcaa cccctaaaac aatatggcgg cgagtaacct 180  
acaacaaaat aaataaaaag aggaaacttc cccccagaaa gagcaacaat tttccacgcc 240  
aaaatacact ttttttgctc gcgctacagg ttgcgtgaga gaacgaaaga gagcgtggag 300  
agagcagcgg agagcgagtg tcaagagaaa agcgcaacaa aagcaggaag cgataaacga 360  
taaatacaca cagcaaaaac gtagcagact ttgcgaaaag aaatttcatt ccgtgtagat 420  
aaaagataca ttaaaatagg agagtatatc ttaatgcaaa ttttttccca tactctaate 480  
aaaaatcaaa atattctcta tgccaaataa tatcgacttt tatttatatt acaaaacagg 540  
ttcttttcag tgtactctgt gcgcatgttt ttttccaatt tgggcaacga ccgcatccaa 600  
agcattacca ccaaacgttc tcttgggcac cagccttttt cctctgcttt gctattcttt 660

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tacttagcat ttctctgggc tatgttgccg caaactttca gagg

704

&lt;210&gt; 796

&lt;211&gt; 307

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(307))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004423. Matches in area of 702AA predicted

protein. Sequence similarity to Xenopus DNA repair

protein XPGC

&lt;400&gt; 796

agttggctca gcaagaagtt ttttgcatth ttaggggttg taagtgggaa atgaaatgga 60  
gaaggtgttg tgtgtgctcg tatgcagcta aaaaatggcg gcaaacacac acaccaaacc 120  
cgaccacac agacaacaaa ggctaaaaga gcagctgttc cgacggcttt ctctagaccc 180  
ggatgaatcaa cagcctccca catccgaacc atccacatgc ccgccccacc atccaattcc 240  
acttccactt ttaacagaag cacacgcacc accggcacgt ggtgcgcat atgcaaatta 300  
agaattc 307

&lt;210&gt; 797

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(412))

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<223> Area matching Drosophila Genomic sequence. Matches  
in area of ORF with sequence similarity to Septin.

<400> 797

gtcgaaagtt aactgcggta ttcgataacg atacgtgttt gctatcgcca ttgatgggtcc 60  
cgttcatggt atcgagccat atttgtccat tttatagcca aacgtttgat tcatttttat 120  
ataatgacat agtttataat catatataat ttcaatgtag tttttaatag gtttgctatt 180  
tctgtaatat atattcggcg aacttagata taacaataga acagttttta agttttaaga 240  
tcataaatct ttaaaacacg cgagattaag acaacgcgat atacgtttac gtaaaggatt 300  
tttttatgga ggtggagaac ttaagttgg cattactgtt caaaatcgcg accgacttaa 360  
catttgccga gttattgccg atatatgacc acaaatgttg gaaaaagtca tc 412

<210> 798

<211> 478

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(478)

<223> Area matching Drosophila Genomic sequence

AC004313. Matches in area of ORF with sequence  
similarity to potassium channel genes.

<400> 798

acagaagccg tcaactcagg cgaagtgtc gtagcggaac ggaatggaaa cggaacatgc 60  
acacgaatgc cagccgaagc aggagtacga agcatgccat cctgtcgtgt gtcagcgaaa 120  
gagaggcaga gagaaccaca actcgctctc aatgggaatg ggtctctccc tctctccctc 180  
tctctctctc totccgcaca acgcctcctg tggtctgttc ctcttccatt tctacgagc 240  
gacaggatgt gcagctgccg actgcgactg catttggtatt cgcgcccccg actccctgtt 300

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actggggatt ttgggatgca ttcccgtaca aagcatacgc atctgggcaa ttcgattccc 360  
ggattgagca acaatccacg cggataacag gactacagga taataggaag tggttgaaaa 420  
atatacactt tatgatttat gatccttaag cggaattta ccacattaaa catatttt 478

&lt;210&gt; 799

&lt;211&gt; 489

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(489))

<223> Area matching *Drosophila* Genomic sequence

AC004641. Matches area of 402AA predicted protein

. Sequence similarity to *Xenopus* FLAP  
endonuclease.

&lt;400&gt; 799

atcgtgacgg tttgctcgcg ctctccgctg cgccgccttt tccgttgcat atgtgtgcgg 60  
gcgttattgt gcatgtttcc ggtggccgaa aaaaaatagn nntatagaaa acagaaacca 120  
agaataataa cagccatacg ataaacagtg tgccaatgtg tgtgtctgtg tgtgtgtgca 180  
tctcgcgtaa caacataatt gcatttatcg gatggcgcaa gcttcaattt aattataaat 240  
aacatgttca actttttata ctattttccc tgcgtcaaag tgggcgttgc aactgcccc 300  
ggaaaatcac gcgccccggt tcaaagttaa agtttgctgg gtaacgcaca cacacacaca 360  
cacaatcact cacacgcggc acacgcacat ttcaataaac taatggagcc tggctttggt 420  
tttggtntaa ttccaaccca cttgagcaca cagcacacac agagaggaaa aatcaatact 480  
cgttatggg 489

&lt;210&gt; 800

&lt;211&gt; 558

&lt;212&gt; DNA

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&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(558))

&lt;223&gt; Area matching Drosophila genomic sequence

AC004306(57408-57954). No good predicted exons in  
this area.

&lt;400&gt; 800

gcaagcacga tgaagaagga aagcgagagc gaccgaaccg cacaccacga gaaattccaa 60  
cagactgaga tggaaacaac aaacgatgac gccggcaatg ccgacgcaca aagcagcgca 120  
cagtggggcg atgtgcggtg gattcgttat ccatcttaaa tagtaatagc ataggcatga 180  
acaatatttt caacaactct tttgcgaaca ctgtaagcag aatgacatgc atttttgcag 240  
aattgtaatt ataattaatt ccggcactaa aattaaatga tttttgttta gtttttaaac 300  
acgatttact tgattcgtaa atattatcaa gtattaatta attacttaag cgaatagtta 360  
aaactggtaa attagcccca aacaatattt taatggtttc aagcccacta tggccaagtg 420  
gcccacctta caaacgaaat ggatccgcat aaaagaagaa attgcaacaa acaggcggca 480  
aggcagccac cgctcatttc aagtcgcttt ggtgggtgctt ctgctggctc tctccgtttt 540  
tagtaattgg ggtgtggc 558

&lt;210&gt; 801

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(623)

&lt;223&gt; Area matching Drosophila Genomic sequence

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AC001646. Matches in area of 724AA predicted protein. Sequence similarity to Mouse serine C-palmitoyltransferase.

&lt;400&gt; 801

```
ggccagttac tcggccagct gttatactga aaactgcgcg ccttcggtat ttttaaggtac 60
ttatcgtatt ttcacatata atttaaaagg ccacattttg tggaacaacg cttccggttg 120
tggtctctgc ttttagtact gccagctcct agcgaatacc tccaccatgc aagcagttca 180
agccgcagtg ctgttttagta tactttctga gcgccagatg tcgcaaaaga gaagtcggtt 240
tttgtattaa ttagattttc aaagaaattt atttaaaacta aaatggtttc tatttttagtc 300
acataggggt tcaacttaaa ttatttgaaa gcaattatta tgaaaaatat ataaattaat 360
atgtgatacg aagggtttta gtgcgagata agctaaaaaa aatgatgttt tatattccat 420
tacatattag aaactacaag ttttcagact taagacgtca agcattttcc ccttgagcat 480
taaaatctgg ccaaaactta cgcaaagaaa aattccgctc gccggcaata ataaattaga 540
ttaaagtgc caaagaaaag gaggaaaaca gaatttcagg ccacaggatt tcagataaaa 600
gtgccgtaag cggcaatgta gta 623
```

&lt;210&gt; 802

&lt;211&gt; 544

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(544)

<223> Area matching *Drosophila* Genomic sequence. Matches in area of ORF with sequence similarity to U5 snRNP genes. *Drosophila* ESTs AA803646, AI518976 and AI108114 come from this gene.

&lt;400&gt; 802

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ctcttgtgtg accgacacaa tgtggtcgca gcagtgtcct atgaaaatac acacacccta 60  
agttaatacc aaaaatatac taaacattta ttttgtccag cacccaaacc attaacatca 120  
gtttttcaac agaactatgt taagcgcagg tgttaactta tattttatatt ataagtggac 180  
tttgttgtcc tgaaacttaa tcatcaccag aatcattatc atgctctcta gctttatttc 240  
tcgtttaact tatgaaaacc acaaatatca aagaccaaca taacatagct ttacaccgga 300  
aaagtatagt agatagtata gcccaaggagt cagctctagc tgtgttggtt atcgttatcg 360  
cggctagcag cttgttttgt tttgcttaca cgacaaataa ataaatataa aagaagtatg 420  
agtaatttaa aatcggacct ggatgaatac ttgctactgc agagtgatca gaagaaccaa 480  
tttcaacgtc aagttgccac agctggaagt tccattttct cagcttcgac ccagaacaaa 540  
tagt 544

&lt;210&gt; 803

&lt;211&gt; 201

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(201)

<223> Area matching *Drosophila* Genomic sequence

AC004154. In intron of predicted gene with  
sequence similarity to mammalian geranylgeranyl  
transferase genes.

&lt;400&gt; 803

gaatcaacta aaaacattta ttaccacct gctcatttat atgctgcagc cctatcagct 60  
gttcgctgcg gcgccacta tcagcgcata cggccacact gcgggggcgg cagggatgcc 120  
aaaaattgat gtggataaca tagaaatatt taaaattgtg aaattattcg attttgataa 180  
gtatacttct taacggaatt c 201

516/586

&lt;210&gt; 804

&lt;211&gt; 524

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (524)

<223> Area matching *Drosophila* Genomic sequence

AC004766. Matches in area of 1442 AA predicted

protein. Sequence similarity to *C. elegans*

ZK1128.2 gene.

&lt;400&gt; 804

```
gtctggactg aaacggtccg ggaaacgagc cgaaagtagg tctgagtggg aaattaatcg 60
aggcacattg agtgaagttc acaaagcttc gccagctttc aggagctttc ccaacaatTT 120
ccccctatTT tcccaaggcc aaaataaatt aaatttttaa atgttaaata cctgtttgtg 180
ttgtgaatgt gttgctgttt ttggtaaagt attaaatgcc aatagttacc tgaaagtaca 240
ataaatttaa ttcaaatacag tggagggtcaa cagtataacg aaacacactc aaagaaatca 300
caaataacga ttaactcact aataaaagga ctttatggat agacatatata actttttcaa 360
gctttgttag ttatggtaag ttatggaaag gagcaaaagc ttttataaaa gcttttcgat 420
tagaaaaagt gttgccagct taaagtatTT ataagaaatt tgaaaaagga tttggtagaa 480
atcttttagag tgaaacatgc caattacggc taatacatgg tagt 524
```

&lt;210&gt; 805

&lt;211&gt; 621

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature



517/586

&lt;222&gt; (1) .. (621)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004361.

&lt;400&gt; 805

cacagcagac tgcgtcacgg atcggatctg tgtggatctt cagttcgggt tagtttccaa 60  
taccaaacc aattccagcg gcattgaaag tgcgtgtggt ttgttgttgc cccatgggct 120  
ttttgtttaa ggtcttggca aatgaaagtt ttctcttcat cgatgctgca ggacattatg 180  
tttgattaac gaaacgcagg tcgagttttg gactgttgta aataaatttt acaaccttta 240  
atgctgccac ccagacaacg taaaaacgag aagcaattga aatgtctgaa ttatgtttgc 300  
tgaattattg aattatatag gtggtcggat actacatgct acatgcatgt aactgaatgc 360  
aagtacttaa ttacgtcagg agaaatttat tttcatttcg aaaaacgcaa taaatgttaa 420  
gcagaaactt caaggggatt taaggagcat tgcataaaca accaaaaatc ctttagatt 480  
tcataaaatt tacaatatct ggtatgattt cgaagactga aatattgatt aaaagaattt 540  
gtacgatttt tcaatcgaac aatgggtcaag cccgatgcc aactcatttt ggcccgcag 600  
taccacacca ttataacaca t 621

&lt;210&gt; 806

&lt;211&gt; 569

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1) .. (569))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC007185.

&lt;400&gt; 806

ctcaatgcga attgttttca agcgccggag agaattctata tagaggggct tctccgactc 60

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gcttcgaata cgtttttcgc agcgcgcgcg ttgcgcatcg aaaatcagaa aagctggcaa 120  
gcgttttaaaa acaaattcgg caggtacaat tgttacatgt tttccctca gttgactatt 180  
tcgtcgcagg tttttggcca gcggaaacca tcgtaataac cgttattttg ttatattcgc 240  
gtaaatcggt gtttggtcaa ccacagaata cttggtgtta cgcatttcga aaatggaaat 300  
gcaaaaattt ccaagcagtg aaaatcaaaa cgaataaaat atattggctt ctttcgtgtt 360  
tagccgcgta cgtgtgtgtt tctgtgttag tgagtgcagc aagaaataaa accaaaaagc 420  
aacaataaaa taaatagaaa acaaaagcaa aatcaaatcc aaattcaaag gcaaatactt 480  
gcaaagtaag ttgataatat caggagtggg ggggtgctagc atatgttgca ttattttgcc 540  
cagcatttac atggttttca caatttctt 569

&lt;210&gt; 807

&lt;211&gt; 462

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

<223> Area matching *Drosophila* Genomic sequence L49408.

Matches in area of 401AA predicted protein.

Sequence similarity to mammalian glia maturation  
factor.

&lt;400&gt; 807

cggcagcacc aatgttggtt ttattgttgt tgtttggctt ggccatcttt tagttgttat 60  
tattgctttt tagtagtgac ctccgacaac aaaccgaaat cgaacnnnca acaacaacag 120  
aaaaaaaaag aactgcatta aagcagagat ttatggtttt ttaatcaaag tctgaagaat 180  
gcaaaggcat tcctttgcc ttagtattgc atttgtaaaa aagtaaactg aaaaaatttg 240  
ggatttatgt ttttcttttt ttgtctaaca aattttgtgc tattataatg gaaatgttaa 300  
tgatatattgt gggtcttggg gaaaatgttt tatattaatt catttcacct gggtatctac 360  
ttgcgtagaa atcaaatgca ataaaaaatt acagtcaaga ttaccaatt gttgcgtatt 420

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ttgagccatt tgtgctttta gacaaccggc ttggttgaat tc

462

&lt;210&gt; 808

&lt;211&gt; 233

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(233))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005750. Matches in area of 1813AA predicted  
protein. Sequence similarity ro Rat CPG2 protein.

&lt;400&gt; 808

ctctgagctt tactacgatt actatacagc tcttctctcg cgactttttg gactggacaa 60  
ggcgtagcac attgaacggc agtggggttg ggtttagtat cgaaccggct ttctacgaca 120  
gcggtattgga agcgcgggagc gacaaagtcg cggggaata atgtgatata gccggctatg 180  
ttcagcaggc aaaactgaaa taaaagtaat aaacaccgaa agcccccga ttc 233

&lt;210&gt; 809

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(525)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005269.

520/586

&lt;400&gt; 809

ccccagccgc gtgcacagcg cacaccaacc gacacactca cagacacacc ccaaagccgt 60  
gtctgagtag ctgacgtagt tgttgaccg gaagtctgtg aacnnngaaa tactttaaaa 120  
ctggctcgaa acctggcaga cgccctcaa gctgaaatct aagacctggc cgcataatatt 180  
tgcattaact ttggaagtct gactttaagc agacacggat ttcattaata aacgaaaggc 240  
atagtgcgaa agcaggagag tatgggagct caacagttga cggggagcat tgccaggccc 300  
aagaaactgg gagataacaa agatgagtca cgaaaagcag gcatttcaaa atcctcttaa 360  
tcaccaccag tgaatgcatg taactcaatt aaagtcgtca attgattaca tttattttgg 420  
gttgaaaacc cttctaggac acgggtaaat tctacctggc aatgcttcgc gtttcgcctg 480  
taacaggttt caaagcaaaa aggggcttcg acacagagca cacac 525

&lt;210&gt; 810

&lt;211&gt; 531

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(531)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence

similarity to Rat fatty acid synthase gene.

&lt;400&gt; 810

gtcggggatc atcatgtctc gatttttcgc ttcagttgtg gagcgagagc ttacgcaatg 60  
gagcggagtg atgagcacat tatccgaggc aattttttan nngccgaaat gccgccgggc 120  
cgttagaaat gaatatgaaa ccatctactt taaatatgat tgtaatgtaa aaacttgcat 180  
caacactaaa aggatctatg gactccccga gcgtatggcc aaaatgaagg actccgatct 240  
ggagaagttc gacgacaagt tctttagcgt ccaccagaag caggcggagc tgatggaccc 300  
ctgcatgcgg atgctgctgg agctgaccca cgaggcgatc atcgatgcgg gcatcaatcc 360

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cgtaacagctg cgcggcagtc ggacgggccc tctacatagg cctgtccttt gtggagacgg 420  
acaccgagat cccaacatg gagccgaacc agtatcaacg gctactggct gacgggctgt 480  
gcgcgtgcca tggtcgccaa tcgcatctct acacgttcga ctttcagggg c 531

&lt;210&gt; 811

&lt;211&gt; 443

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(443))

<223> Area matching *Drosophila* Genomic sequence

AC004758.

&lt;400&gt; 811

ggctcgcccc aagagagccg agtgaaaccg agcgcgcacc cgaatgccga aaatcaagta 60  
tacgtcgcta cgategttgc tcaccgcctt tcagtgtctt nnncaataac aaaaataata 120  
gcactgctaa acggaaaaca gaaacgttcc tcttctaacg gtctcactga gttttgtaaa 180  
ttggtcattg gctgtgcgaa aaggagagac agagagagaa ccagagaact gtcgcagcga 240  
ttgcgattac ggttacgcgg cgcagtgaaa aagtgaataa gtttaggcgg aaaacacttg 300  
cctctggctg atttgctgtt ttggacgcgc gactccctca gaacttgaaa aataaaggaa 360  
aaatcggaat ttaagcaaaa aagtgatcac acatcaagaa gccaaacttg attacgattt 420  
gcggtcgaga aggacttata aac 443

&lt;210&gt; 812

&lt;211&gt; 498

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

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&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(498))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005894. Matches in area of ORF with sequence  
similarity to metalloprotease genes.

&lt;400&gt; 812

gtccagcctt tcgaaggag tgcgtgggtg ggtgtgtgtc ttttttatta aatgtttgcc 60  
gtggtgggcg tggccatcac tcgagccgct agctggcaca tcctttttat taaaattcgc 120  
agtctataaa ttgctaagga gcccatgtgg gatgggcggg cgtgggattc caatggccat 180  
gggactgcga tgagcggagg aaatggggta tgactggcgt acatgtttca aaagacgtgt 240  
gtgtacccaa gacttttatg agacagcaac aggaaatgca tggaaatggt ctgggctggg 300  
ccgcccgcgc agaaagggga acgtgtgttt ctccaaatgg agcagggtcaa aaaacgaatg 360  
tgggaagtcc gaagaatgat tcagaaactg aaaatatatg aataattatt acaaaatctg 420  
ccttgcatat aattacttat aactttgcac tagttgcatt aaaaaatgaa agatagtcga 480  
ccgaagtttt taagcctc 498

&lt;210&gt; 813

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(320)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004564. Matches in area of ORF with sequence  
similarity to Immunophilin genes.

&lt;400&gt; 813

523/586

ttgtaaatga agcgaaaagt caaagaagaa gcagaaacca gcataaaaaa tgtttgtgcg 60  
ctggcggtt gtaaaagtat gtgtgagtgc gtgcgtgtgt gtgtaggcag cagacaactt 120  
tgaagaagaa gagacagaat acaaaaacgt acggagtctg aaaactccgc cagagaagtt 180  
tgtctacact gtgcaacaaa ttaggtggga atgggatgtt atcttatcag gttgggtgta 240  
ttggttataa ttggcggcc aattgggtta ccaaaaaatg tgtttaaaca tcagggttaca 300  
tctgaaaatt ataataaatt 320

&lt;210&gt; 814

&lt;211&gt; 429

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(429)

<223> Area matching *Drosophila* Genomic sequence

AC005716. Matches in area of ORF with sequence  
similarity to follistatin genes.

&lt;400&gt; 814

ctccagactg tctgtttggc agtgcgagtg tattggtgta cctcctctgg tgtgtgagtg 60  
tgtgtgtgtg tggaccctga gtttggcaat gcagttgccg aggnntgcc ttgttgttgc 120  
tgcgcgctc cttgcatttt ttcgcgtgc tgctcctgta ctcttgctgc cccctttgt 180  
tatttgtgct gtgccccaaa gacatttcag cgagcctega ggaatccaaa gcatttggat 240  
acgaaaactt tgggtacagt aaaggctgct gggttcccgc caaacagtgg aatgttatgc 300  
cttagccgga tcattcgca tcggtgctga aatctgcggc tcattatcta agtatggcca 360  
gggtggaatta acactttcac cgcactgaca gaaaaacatt ggccttttta aggggaacca 420  
aataataat 429

&lt;210&gt; 815

524/586

&lt;211&gt; 71

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(71))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC007180. Matches in area of 217AA predicted  
protein.

&lt;400&gt; 815

ttccaacggc tcgagacagt ccgagcggca cttgcaacat gttgcaagtt cgtgtgtgac 60  
ttcgggaatt c 71

&lt;210&gt; 816

&lt;211&gt; 75

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(75)

&lt;223&gt; Area matching Drosophila genomic sequence

AC004758(92123-92197). In intron of gene at  
87648-113518 coding for 945AA protein similar to  
Human retinoblastoma binding protein 2.

&lt;400&gt; 816

aaactataca cacacacaca tacgcacgca ccgccagtca gtcaggcagg cacacattgc 60  
ccacccactt ttact 75



525/586

&lt;210&gt; 817

&lt;211&gt; 116

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(116))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC001661. Matches in intron of Drosophila wing  
blister gene.

&lt;400&gt; 817

atctggctctg aagtgcagcg cttgcgatca gttcgtgttt gacggtcggt tgcgtaggaa 60  
gcaagacacg cgacgggtct cgagtgtgtg gctttgcctg tgcgatggct gaattc 116

&lt;210&gt; 818

&lt;211&gt; 512

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(512))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004758. Matches in area of ORF with sequence  
similarity to Human Retinoblastoma binding  
protein.

526/586

&lt;400&gt; 818

cacagtttct tatcggcgga ggtcgacgaa tcggatctcg tcttatcgcc gaccccccg 60  
ttattgtttc gtttctgtat tagattcaaa atcagttcgg tgataggcgt tactcagtct 120  
agccggcgcc gcgtttaaca ctatgccggt tcagggacag gacttgaaac atccatagga 180  
tccatcgagc atatacgcaa ggttttctaa gtacgctttt ttaattaatt ttatgaaatg 240  
tgtttcaatg cagtgagaga tgggtttttc aagacttcgg taagctaaaa aaggaaagtt 300  
tggcattcta aaagagtggc ctagaattat attctaagtt attaataataa ggtaagtga 360  
ctcttttatt gtttttagaa tactgggtgtg tgaaattaaa ccttggcttt aagaatttga 420  
atttgtataa tatatttaaa ataactagta gacataagta tttagttaac ggtaatgcct 480  
atgaaatggg gctgctcact caacaaccac ag 512

&lt;210&gt; 819

&lt;211&gt; 54

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(54)

<223> Area matching *Drosophila* Genomic sequence

AC004334. Matches in area of 433AA predicted  
protein.

&lt;400&gt; 819

gtctgatgca gctgatctga tttattacca gtttactgga tcactcgtga attc 54

&lt;210&gt; 820

&lt;211&gt; 557

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

527/586

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(557))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005149. Matches in area of 424AA predicted  
protein.

&lt;400&gt; 820

cacgaaccca agaaacaggg cccgaatgga aaaagagaga atcgagagaa tcgcgggctg 60  
agaaatgcgt agaaagagac aagcgacgag tagcgagcag tggcactaaa accagcttag 120  
tgcactgtgg aaaaagtfff aacaattctt aaatatctga agagtaaggc tctaattttc 180  
tgtaaataac aacagtataa agctatgtgt ttaaataaac tagataaata atggatgcat 240  
ttacatatct atctgaattg gctagttact tatattcggg ttgaaaatag taaaaaattt 300  
ctttcagtg gaggagaggaa ttaaaccgaa ctcaacccaa acccaaccgg ccgccagtcg 360  
cacgctgcta aatggacgga tgggcccgtg gacggactta tatggagact ggcactggcg 420  
gaagcgtggg aacgtgcatt cgtacgacga gttattggca gttagagcgc tacctgttta 480  
ccgacccgac tacccgacta ccaccgactg cttttttttt ttggcccatc gaaaaggtag 540  
ggtacaattg gcccggg 557

&lt;210&gt; 821

&lt;211&gt; 202

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(202)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005333.

528/586

&lt;400&gt; 821

tggcaggcct ttgcatttcc acttgtgcgt cacgtgctcc tggctgttgt tgttgattg 60  
aacttgaact agtggcaaag ttgttgctgt cgttgtgggt gctattgcac ttttgcgtgt 120  
cttccgacat tggcgccctat tttgccggct gtttttggct ggcattcggc gcgttttctc 180  
accgcgcacg cgctctgaat tc 202

&lt;210&gt; 822

&lt;211&gt; 534

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement ((1)..(534))

<223> Area matching *Drosophila* Genomic sequence

AC005334. Matches in area of 309AA predicted  
protein.

&lt;400&gt; 822

ctttgtgcgc tgaagcagca acaacagctg gctatctcgc tctagcaacc acgtcagacg 60  
gcaaacgtca attataagca aacaaagcga cgttgcctca tttcacgaaa gccgcagcga 120  
ggcagagcga gagcaagcga aatggcgctt cgcggcaacg ttgccaaact tcagcgtcga 180  
ctgcgtgttg ttctttagt ttccatgctt ctttagtgca tggaatttta acatgctgta 240  
ccaccaaccc tctttacggg ggatggggga ttataataac gcgctgctga cgctgctgct 300  
cgcattttcc accttctcgc attcgtattg ttgcaaagga aatgggccct atacaagaag 360  
tttatctttg aatatacata catacatatg tatatttaag tacatgccgt attccgtgct 420  
taaattgagg cacaggagga gaacatatct tgggggccat tgaaattcaa taaattaaat 480  
gctctagtga ataaataaaa gcgtatttta agtgggaaat aagcaatgcc atta 534

&lt;210&gt; 823

&lt;211&gt; 438

529/586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(438)

<223> Area matching *Drosophila* Genomic sequence

AC006421.

&lt;400&gt; 823

```
cttgtccttc tcagaacaac agttataagc tcagtctgcg ccggcagcgc tgcgacgtc 60
gactgcagca gcagcgccgc tcatttgtgc gcttaatgac gtcattatTT ttattttaac 120
agtgccaaagc aaattgcata tataccgttg ctgctcctgc gcagtcggcg ctctgccggc 180
gtcgctgcac cgccagtggg gcttgggcta ggggggtgggc gagagagcga cagagagaga 240
gccagagcga gagagaacga gaggcagtga gtgagagaga ccccggtcgc tttctcgctc 300
gcacccgctg agctgggcct gcggcttcgg gttcctcgcc ttcgttctgg ttgcttcgtg 360
tttgccgatg tgatgctgct gatgttgctg ctgctccttt tgctgtgcta cttatgctga 420
tgattgcgat gctggggg                                     438
```

&lt;210&gt; 824

&lt;211&gt; 524

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(524))

<223> Area matching *Drosophila* Genomic sequence

AC005443.

530/586

&lt;400&gt; 824

ggcacggcat cctttggcgc gagagaatgc gacatccgga gagccggaga gcacgaccat 60  
tgagggtcct gttcgggaga gctgacgcct ctgtgtctaa ctaaaccgaa gaggctcaag 120  
gcgtcgcattg atacttccac agtcatctca atttcaagac tagaagggtta aatagatctt 180  
tatttatatt atgattcaat taaattatta attttatatt tcaaataattt aaaaaaagc 240  
cttatgggtta tgcctttaa atatattatt ttttaatttaa gttataagat agaaaatctt 300  
atatggagtt cttaaattatt attcataaaa cgtaagtggg aacatgtgaa ttagttaaac 360  
aataagtggg actctctggt aaataaatac attttgcct gaattggatt acaaaatcac 420  
tcgttcttca aaacacctca aaatcaattg aggtctccat ccttttcggt atgccgctg 480  
aatcgatttt cggaattcg cgccaaatac cgcaccgac aatg 524

&lt;210&gt; 825

&lt;211&gt; 492

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(492)

<223> Area matching *Drosophila* Genomic sequence. Matches  
in area of ORF with sequence similarity uridine  
phosphorylase.

&lt;400&gt; 825

gtgcagttcg cgtaccagca cacacaacac acacacacat gcatgcgtac atacgcgcgc 60  
gctaagtgaac tacatacata cgtatgtatg gacgtacagc gtgctgagag gtacagtcgc 120  
cgctaattggt gaaaactggc tgtgcgaaaa agcaggcaga gagcaagagg aagagagagc 180  
gggtcccgggg tggggtggca acttcaactt tgccggctgc acttggaac aagtctgcaa 240  
gcgactgcga ctccaattga ggggtcaaggc cagcgcctgc gcatcagctg ctgcgcattg 300  
gtgacgacca cgacggcggc cgtgacgcga cgggtggcttc gcgaaagctg cgctccgagt 360  
ttctggagcc cgcagtcgga tgggcaagaa cagagaaccg gttgcaagcc cggtttggtc 420

531/586

actttttgcg cttctcatatc ttaagtgcgg tgcgatcgcg ggctcgtccaa tatcgccgat 480  
ttagttaggc ta 492

&lt;210&gt; 826

&lt;211&gt; 535

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(535)

<223> Area matching *Drosophila* Genomic sequence

AC005889.

&lt;400&gt; 826

gtccagtcta caaacagaaa gaatttcaac ggcacgcgctc gacaataaag taaacaaact 60  
gaaattgttt tccttcgtca tattttcctt tctcttgtct cgtctgcgac ttgttgaaac 120  
tatttcaagc gcagaaatca acttaagccc cagctaccca gctcatcaat aacaacatcg 180  
caacatctct ggcgctcaat taacatgggtt ttgtgaaaat ttattgaatc ccttctttaa 240  
tgaagtgcc a tgtcccgaag gctgttgctt cccttccagc caaacgtgct catcgattgg 300  
aaacgggtcta tggccgttta gtttgggtgc tgataaacct agattcagaa tctttagata 360  
tatatcttta gatttatact ttcttgtgta attgaatttt ctaaattctt attctactgc 420  
ccaagtaatg aaaattccca acaaataacg aaggcaagga tatcatcgct ttcttggttt 480  
aatcaatcaa acggcaaacg gactggaaag aagtgatatc agaaatctgt aagtt 535

&lt;210&gt; 827

&lt;211&gt; 47

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

532/586

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(47))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005130. Matches in area of 826AA predicted protein. Sequence similarity to Helix-loop-helix genes. Drosophila ESTs AA949050 and AA817663 come from this gene

&lt;400&gt; 827

gcttagccat attacttggt tgtatttgca aaagttgtaa tagattc

47

&lt;210&gt; 828

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(551)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005554. Matches in area of ORF with sequence similarity to Rat fatty acid synthase.

&lt;400&gt; 828

atacgcccgt tcaattgctg taaaaggata gttctcacca tcgcattgcg agttttattca 60  
ccggtagatc aaccgatctg gagagactat gaaaataata cttcaatgaa cttgagaaat 120  
cacgccacct tatctcacta aacaaatggt acacgcgtcg agctcgtgtg tctgtgtgtg 180  
tgtgtgtgtg tatgtacaca cacatggcgg tggggacttt tggggctgcg tcttgactat 240  
acgccgctct ctttggcacc cacctccgat ttggatgccg actacaatag caaacataa 300  
acatagaagt ctggccaagc caacggccat ttgatagata agcttgctgc tgagtcgccc 360



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gatttttacc ggcaatttgt agtgggtaca cgcggaaaaa taggggtatt atatgaaaat 420  
ggttcctgta aatatgggtc catatttata tgatcaataa catttgaatt tcaaagaact 480  
ctacgggtac acgattcgaa ttcgtttgtc tgagtggact ggttatttgc tctgtgtgtg 540  
accgtcatgt c 551

&lt;210&gt; 829

&lt;211&gt; 499

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (100)

<223> Area matching *Drosophila Drongo* gene.

&lt;220&gt;

&lt;221&gt; intron

&lt;222&gt; (101) .. (146)

<223> Intron in *Drosophila Drongo* gene.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (146) .. (499)

<223> Area matching *Drosophila Drongo* gene.

&lt;400&gt; 829

gtcgcgctat tttgtttcga gtgcgctgtg ctgtttgggt tcgttccgtt tcgtttcgtc 60  
gttcgttttc cattcgtctt cgaatccgca ctgcaaacaa acaagaagag ggggaagcag 120  
caaaagtggc gagtgcattc gcagcgctga aatttcaatt gaaatctgaa atctgtgtgg 180  
caattgcagc ggcaactcggg gtaaatagat tgaattgaag cgaaattctg cgagtcgaag 240

534/586

aagtgaaaag taaacaataa cacgggcaat cggaaaagtg gttttcgata aatcgaccg 300  
cacacacaca cctgtcagtg tgagtgtcaa agtgagtgtg tggagtgtgc gtcgaaggag 360  
aggaaaggtc aagccaaaat ttgcgtaaag aaaaggaaaag gaaagcttag aagaggggaa 420  
aggggaatta cgtcagttcg cattccgata aaaattttga ttccttaaac cgatcctgat 480  
agccagcatt acgatggca 499

&lt;210&gt; 830

&lt;211&gt; 580

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(580)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase.

&lt;400&gt; 830

gcttaaaccg actccgccag ctccgctcat tatatagttt cccttctttt gttgaatcat 60  
tcgatttcgc acatcgtagc agtttctcgg cgaataagaa agcagcttgc cgttcgcggt 120  
ggctcagtgt gagtgtgtgc ggcctatgtt aacgcgaatg gtgttgact gttaacgcga 180  
ctgccacaag ttgctgttaa ctgtcaaccc agtcgctggc ttcaaagcag caagccgccc 240  
ataacaaata atgctgtgtg ccggtatatg cgcagtcaaa gctccgactg cgcggcatca 300  
cctgatttgc aatttctaca ccaactttcc accagctgaa cattcaaaca aaaaacctaa 360  
tcgcccggca tcccgcgcca gagagcgaaa gctctgcgct tgcgggtggt aaagagcttt 420  
tgcttaacag cgaaggggtg gcagacaagt tgcagatgcg gcagaatgat cacaatttta 480  
aaatatttaa tacacgaaat gagttatact aaccagactt tcgcatcctc ttctccaatt 540  
gcagccccta cactaaacct gtgcaagccg tggaccaccg 580

&lt;210&gt; 831

535/586

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(256))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004722. matches area of 834AA predicted  
protein. Sequence similarity to bromodomain  
containing proteins

&lt;400&gt; 831

gatgagatgc caccgagcg gcgattggtg gaggtcacca tgttttgcgt cggcttctgc 60  
agggcggtcg acttctgag actcgcttg ttggcgccac tgaatagggt gcgcgtcgag 120  
ttgaggctct gcagcgaggt gtccagcttg ttgcgaatcc tgtccagatc ggcacgcatt 180  
cgctggatat ccategctat ggtgtgtcga tcgctttgca gcttcttgtg ctgctgcaac 240  
atggtctcca gcactt 256

&lt;210&gt; 832

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(406)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC003054. Matches in area of 822AA predicted  
protein.

&lt;400&gt; 832

atctggattg aggtcttgcc acagttagcc gagcaaagcg cagctatacc aattctccat 60  
ggcgcgtctcg gccacagtgg gtcaattctc catgctccac tctgggcaat caatttctcg 120  
atattgttgt gcagtgcacg tagattgagt cactcctcct cgcattcggc attcccattt 180  
gtatatatat acactcatat tcgtaattat tgtaatgagc catttctcta gttactttcc 240  
tcgttggctg catgggctgg gtttttaatt aattttccat tgaccagcc tgacagctga 300  
gcctcagctt tttcctcttt tatttctgag ctgagctcag aggctctgcc agcccaagag 360  
catttcatat taattctcat tttttcgggc tccaattcgg ggcttc 406

&lt;210&gt; 833

&lt;211&gt; 460

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(460)

<223> Area matching *Drosophila* Genomic sequence

AC004280.

&lt;400&gt; 833

gcccacccgg agcgcattgt gattgatgag cggagagagc gagcgagagc gcggtacatt 60  
agcattaacg gcgcatgtgg cgcgaaaatg cggatggaat caccttgtgg ttgttgttgt 120  
tgccgcgtgc accaccctta aagaacttgt tttgcactga cagaaatttt gagccgcccg 180  
tggctggaaa aatgcaattg caacagtgc cgtggataat tgggaactcg aactgcgggc 240  
cggggtgcgc aggtaaaagg cgcaggtgca ccggagcgca gatacaggta aaaagtgaag 300  
cggttatcct gaggaagaaa caagtaatca tgcttgccg tggatcgtct atttgaagtg 360  
taaatatgta ttgtaatgca atatggtatg tattgaagtg tgttggtatg aaggaaagca 420  
ggccggaata ctgattactg ctaccgtatg taggcagatt 460

537/586

&lt;210&gt; 834

&lt;211&gt; 99

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(99)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004722. Matches in area of 289AA predicted  
protein.

&lt;400&gt; 834

ctttgaatga aaacaccgaa tagcatataa aatgcatttg ctccttagta aaaaagttaa 60  
gaagggtttgc cgctgttttc gtattcgaat tacgaattc 99

&lt;210&gt; 835

&lt;211&gt; 178

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(178))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC001661. matches in area of ORF with sequence  
similarity to Mouse Surfeit gene.

&lt;400&gt; 835

gtccttactt gcaattcatt ttcgaaagaa tcaagttggt tgcttttatt gaaagtctgc 60

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agctctgaaat taattgaagt gaagaatata aaggccttgc ttactcttga ccaatctcag 120  
gtaagtataa accattatag acggactaag aaaaggcaaa gaatctgtag gtgaattc 178

&lt;210&gt; 836

&lt;211&gt; 602

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(602))

<223> Area matching *Drosophila* Genomic sequence

AC005269.

&lt;400&gt; 836

gcctagccaa aagctaggca aacaggccaa gcccacccc ataaaacccat gtcacatttc 60  
tggctcgttt tttatctggc caagaaagaa acaaacaaac actgtcgcac attagagcgc 120  
aacgtgccga gcccataaaa agatttcgac gtcttcgcac gagtcataat acaccctcgc 180  
cattcgctt ccccatgaaa tcaccacct gaggcacgtc ataataatat tgggtggtgtg 240  
gctgcatttt ccttgcatgc ttttaggcgc aatttttaaa tggttctaga atatgcgccg 300  
aaaacgcaac agttgctcat gttttcatcc ttaaaaatta agtagtgaaa tttgaaaagt 360  
ccatattaaa aacagttttt aaaattttta gacatttttt gtttctgtca ggagcacatc 420  
aatttaaaga cttttatggg ggtcatcaat acagtattca cttttaacat ttacattacg 480  
tctataattt aaagcacagc tggcagcaca gttaatgagt aatattctgg caccctaaac 540  
ggcttaaaaa agttcaaaac cgcaaaacaa ggtccttggc tttcaaggac atgacctggg 600  
tg 602

&lt;210&gt; 837

&lt;211&gt; 562

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

539/586

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (562)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004362.

&lt;400&gt; 837

cgacggacct ttcgaaaact tgacgaacac gaagcagagg ttcaaagcaa aatggagtaa 60  
acgagtgaag aacaaaataa tgaattatgt caaaagtggc gcaaatatct ttggtacacg 120  
aagaaaaaga ttggtagtgg catttagccc ttaccacaaa tctacgtaca tacatatgta 180  
tgtatgttta catatgtaga attattaata gtattttaat tattgtaaaa tcgtgggttat 240  
atatttttt gtgagtagtt actctatgta cgtgctccca accaatgagt gagcgagata 300  
gactgctaag tggagaatgg gagttcattg atatttctcg ggcgttttgc tttcgcttcc 360  
ccttcgtctc caccttgctt cgcgccatct tcgttctttc ctcttctcct ctgcttccat 420  
ttacctgcca cattcatttt gtggtggttc ttcgcaattt tgctttcttc ttttaatttg 480  
cattcttttg gacgtttttt agtttgcggg tcgcttttgc gccgttaact ttggaccgtc 540  
tgcggggtgt ctggtgtgga tg 562

&lt;210&gt; 838

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (521)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004370. Matches area of 1277AA predicted  
protein. Sequence similarity to human nuclear

transport receptor.

<400> 838

gggccgtcta ttttaagcact gcctctcgag gagagagtaa ctttctttta acgctctcgc 60  
tgctctcttt ttcgctctcc ccgaaatcgt tacgacgctc actcgtctctc tctctccac 120  
gccattggcc catacaatac actcaaaaaa tcgccgcggc atttgtacag ccgcagtcga 180  
taagacaaca acaacagccc agagcagagc gatcggttga tttttggtat attattttgc 240  
ggtgattttc tgataatata gtatctatat agtaaggctt tagggagggtg ccatatatca 300  
ggcggcgcta cggcaggcaa aaggatttac tcgtaggccc cacttgatgt atggaataat 360  
cccgttttcc tttttggttt gctaaccacc ggatatgtgc ttcccgtcgg acgggttcgt 420  
acaagacttg actttgcccg gtccgttcga tggcttagaa attgccgctt gcttcttctt 480  
gcgccaaaat cgggtgcata cattttcgtc atacttgata c 521

<210> 839

<211> 619

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(619)

<223> Area matching *Drosophila* Genomic sequence L49408.

<400> 839

gttgtgggtg tgcgcgagcg tgtgagctat agctctcatt ctataaaccg tatctctagt 60  
gcaaattgtgt gtgtgtaatt cgagtaaagc cggtagaagt cgcagctggt tttgcctatt 120  
tttacgctca cacatatctt gcaacaaaga aaaacaacaa ttctctagcg gcgattttat 180  
ggctcgtgca attcgtctca gggtccgtta tgatcaaaaa tatttggtatg ctaatttttag 240  
caggctgccg ttactaataa atacgaaatc gtgtttaata gtccatcata gcgaccta 300  
aaatatatc aggaaataaa cggaaacaac aagtgaatat atgcataaat agttgttgat 360  
ttcatagctt agcataatgt ttttcaaatt tcatttatgt caagtatttg aactgaaatt 420



541/586

tttttcggtg caccgaaca caccgatttct gctatcttct actttggcgt ggccatagag 480  
ctcagccaaa aatttgcaca aaaattaatg tcagctgact tgctttgggt cacttctcat 540  
tttcgtggcg cttcacacac acctggcatc atctgcaggt gaagagtcga aagataagcc 600  
agaacgctac gttaatggt 619

&lt;210&gt; 840

&lt;211&gt; 535

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(535))

<223> Area matching *Drosophila* Genomic sequence

AC005447. Matches in area of 802AA predicted  
protein.

&lt;400&gt; 840

ttccgtgcga ttgccgagcg gtaagcggcg agcgtctaaa cgctcactca ctcacacact 60  
caagttcata ttttgtatgg tacagtgggc ctgggtgcga gatttcgtcg aggggcgcag 120  
tttggttttg caatttacca atttacaggc gttttgccgc ccaaactgcc caaatcgccg 180  
aactaagctg ggagcgtgac caaatcaatc gactgttcag acacagcatc ttgagtggtc 240  
ttgtaagtaa gacatttacg ccaattttcc aatcaccaaa cctgttggtg agcaacagcc 300  
gccaacgggtg cgtatgatta atgcctatcg ctgtctgtca tctgagctga ggctgggaca 360  
atgggcagcg cagcactcga aaaagtacct ggcaggcgct gtatcataat gctctcgctg 420  
tcatcggcac ttcaatagct aaaaaaacct tatcaaagct ttaaggcctt atcaccgaca 480  
aactgactct ttggcgcttc ttatcaacca ccattggccg cgatttcagt gagtt 535

&lt;210&gt; 841

&lt;211&gt; 342

542/586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(342)

<223> Area matching *Drosophila* Genomic sequence

AC004120.

&lt;400&gt; 841

```
ccaccaacca agccacctac ccgccatctc gacgatgaac tgtcgcgctg tttgctgcca 60
tttctgtccg ggcttggtat tgtttaactg gcaatgatta atggcaatga ggcagggcag 120
agcagagcaa aagcggagca agaaggtggg caccgagttt tgaactacac aaaacggaac 180
atcatcacat cgctggcatt tctttttgcc agtgaccag aaacatttct tcgccagctg 240
ccattcaaca cttgaggggtg attagaattt gcgccatcac tgaagcgggg gccgataaaa 300
gcggagcatt ttattgattt gtctgactca ttggatgtgc cg 342
```

&lt;210&gt; 842

&lt;211&gt; 512

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(512)

<223> Area matching *Drosophila* Genomic sequence

AC005454. Matches in area of ORF with sequence  
similarity to mitochondrial translocase.

&lt;400&gt; 842

```
gtacacggtc gacaacaaca aatgcagtat agcgaacgaa tgtgacgatt ctattatgat 60
```

543/586

cgtttatgtt cggttataag gcgtggaaaa gtgtcatcca ttcccagaca tctagacagc 120  
caaacttaag atcatatggc tgcgttctag acattctgaa gaaagccaaa aacaaaagca 180  
tgtattcagc aaaagtcgac aagacatgag taactccaat cgaaatattt ggggtataaa 240  
cccaaaaact ggggtgtattc acttgtgtac tattacctca tgtcttttta ttctttttca 300  
gatactctac gcgttaatac accttctgta cacattgctt aagttggaaa atgtatgttt 360  
atggagccta atataataat tccattgttg ttgttaaata acgattacat atttaattat 420  
gtgcagcaag ataaataaat tattcatcac accattgtca ccgtcacaat atcttaaggt 480  
tttggttaatt catataaatg gtaataccat ca 512

&lt;210&gt; 843

&lt;211&gt; 515

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(515))

<223> Area matching *Drosophila* Genomic sequence

AC005130.

&lt;400&gt; 843

ggctgcggga aaccaggaag agatatgatg gtggcggggg cgtaggggaa tggaaaagca 60  
gtgtagaagc aaacgtcgag cgacgtcacg caaaagttgt ttgcgttggc gaatagagcg 120  
caaaagtagg caacgttatac tgttcattgc ggtgactgtg tgtgcggtaa agtgggtcgg 180  
tgggtggaat gtttacacac atgaccctgc catgggagta tgcgtggttg tgagtatgtg 240  
aggcatgctg atgagttctg tatgttgttt ttcttgaaca aactttaatt gtttttgatt 300  
ttcctaagga ttcaagtgcc gcgagtttta ttacttgttt gtttactcat ctgaaggatg 360  
atgcatagag gtgcggggac agtttgcctt ttagaagcct tttcaaagc cagttggta 420  
aaaaaatgag aaagcggaaa ggggcataac agaaatgggt ctctcttggc taattagatg 480  
agcgttgttg tgcttcctg aaaaaagggg aattc 515

<210> 844

<211> 499

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (499)

<223> Area matching *Drosophila* Genomic sequence

AC005439.

<400> 844

```
gcttggcggc aaaagaatga agcacgacgg ccgcagagag aacaaggcag cgaagagaga 60
gcccgcgctc tcttaggcgc tctctttcgg ccacaaggca ctcggtggt gcattgacct 120
cacagctcgc tgacccactt acgaagctgc tttttgccac tgcgaatgcg agttgcgaat 180
tgcgaaactgc cgacgctgcg agctcgtgcc tccgtcgacg ccgctgccgt catcgttgct 240
gggtgtttctg tttcgacgaa cgagcaactt gtgcaatagt cgcagcagca acagcaacaa 300
gagcagcaac aacaacggct gcagcggcaa cagcaagcaa ttcgcagtcg cagcagaggc 360
gactgcgctg ccacatgggc aactcaaaat tggactgtgc ttcactcttt gctagcacag 420
tggttgaaag taaggcgttt aataatgata aataatatat atgcattatt gaatgaaatg 480
gaagaataga ctgcagggg                                     499
```

<210> 845

<211> 565

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1) .. (565)

<223> Area matching Drosophila Genomic sequence

AC005127.

<400> 845

```
ggtaccacgt ttgtgttggg gtgaccgacg ggggggatgcg agaaaatacc accaattaat 60
acaaataggg ttaaaatacc aattagcgtg tacacaatcc acaattagcg tggacacgca 120
ccgaaactat ctttttagcca gtacaacctc caaagttatg acgattggta acgccgtttt 180
cgacttcgaa tattttagtg tgccaacctt cttgaagatt gtatgctgctc gtgaatttaa 240
atTTTTTTTaa atcgtgataa tgcgtcgagc aacaatctaa gctaaaatta gatggcaccg 300
gcgtttattg atgcgaaaca tatgcaatgc caacaatctt aatatgattc tatgcttttag 360
ctctttgaac ctttaaagt tggccaagca cccaaagtgt tgaactatag catgtgtttt 420
atttaaaatc tattttagtg agagcttaaa acctaaacag tgggggtgtgg gattaaggta 480
tctacaactg cgtgattgga agagaccag ttgctttgtg acggtcacaa cccgatgctg 540
tgtcaagctt tacgctttat gataa 565
```

<210> 846

<211> 586

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (1)..(568)

<223> Area matching Drosophila Genomic sequence

AC005889. Matches in area of predicted gene coding  
for 1365AA protein. ESTs AI106939 and AI296430  
come from this gene.

<400> 846

```
ctttgcaccg atgacgtatc ggctatttgc aatttcacat agttgctgatt gcgtttcgtt 60
```

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ctatatattggt ctaaattggt gtcgctgccc ccaactcacac atacgccctc acaaaacagg 120  
tgcagaatgt gataacacac acacacacac acactctccc gccgagcaag ccggtaaaca 180  
aaactggaaa gagagagtgc cagagagcaa agcttccttt ttttggcaaa gagcgcgaaag 240  
aagcttcgtg ttgccattgg tggtcgacgc cgggtgggtg ttggtggtgg tgtcgttgag 300  
cgttttttta cacaattgca ttcaaaaaat gtgtgcttag tatttcggca actttgtgac 360  
tgagcgaacg ttctgtgttc tctgcttttc attatttcgg agatttttcg agagtaactt 420  
gcgatttctg gcccggaattg agtcacacat ttagagccta gaccgtgata agacccgaaa 480  
aaaatattaa acataaaacg caagtaagag gagccacgag aaaccaaaca aaagtgaag 540  
ccattgacat ttgtcctgcc aagtttgaag tgatgacctt gaattc 586

&lt;210&gt; 847

&lt;211&gt; 503

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(503))

<223> Area matching *Drosophila* Genomic sequence

AC005558. Matches in area of 1277AA predicted  
protein. Sequence similarity to human nuclear  
transport receptor.

&lt;400&gt; 847

tctcagactg aaactcgaaa taaaaatgta cagtttaacg ggagcgttct ctgcctctct 60  
ctctctctct ctctctccca ggagaaagat agatacaa atagagcgcgt gctaactctc 120  
tccctcgtaa tttgtataca caccgttttg tctgtttgcg tatgtgctta catttatctt 180  
tcactttttt tctgctctgc cttatgcgta tttatttttag tacataaaac aagacggcta 240  
aacagggtgt cgcaaaagtt agttgggttt ctccgggatt caattgaata atgatcatta 300  
tcccatgata atgaattagt tgagatacgt ttggcacgga taattcttaa gtggtacagt 360  
aacgaattgt atagatttca agaaatagtt ttgaaaataa ttcgttgctt tccatatctt 420

547/586

tcgattccaa ccaccagatt actttgtcct ataaaatgta tcttcaccct tagaaacaca 480  
acctaaacct ttactaatca gaa 503

&lt;210&gt; 848

&lt;211&gt; 620

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(620)

<223> Area matching *Drosophila* Genomic sequence

AC004351. Matches in area of ORF with sequence  
similarity to LUN/Forkhead genes.

&lt;400&gt; 848

tgtctcttgc cgaccctacg tgggctggaa gaactcgggtg cgccacaatc tcagcctgaa 60  
cgagtgcctc aagaagctgc caaagggcat gggcgtgggc aagccgggca agggcaacta 120  
ctggaccatt gacgagaact cggtcatct cttcgaggac gagggcagcc tgaggcgccg 180  
gccgcgtggc tatcgctcca agatcaaggt gaagccgtat gccggccatg ccaatggata 240  
ctacgccagc ggctatggcg atgcgggaat ggtaagctcc atcgatttca taacaactta 300  
agatcatata atatctatag tacttctctc ttgcccacc aggacaatgg caactattac 360  
gcctcgctcg cctttgctag ctacgattac agtgcagctg gagccacttg gcgtctcgcc 420  
ggctgggtgg tcaaggattc gcccgatccc tggaacgccc atgccggcca cagtggctcg 480  
tcgtccggtg gggccgtggg catggggccg tgggtcccct ggcccagtat acgaacatat 540  
ctggctggca gccggaggca atggtgaatg gctcggctac acgccccgc tgggccactt 600  
cgactggga atgggcccac 620

&lt;210&gt; 849

&lt;211&gt; 519

548/586

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(519))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004766. Matches in area of ORF with sequence  
similarity to Lipase 3 genes.

&lt;400&gt; 849

gcgtggatgt acctgctcga gtaaataaca tcgatgaaaa catcgataat atcggccttgg 60  
gtattgtcgt gacacacgca cagtgggtgca ccacacatcg gttcgttaaa atataaacia 120  
atataaatca aatTTTTtga tttaaaaaaa agtggttaacg taaactggtc aatTTTTatat 180  
tctgctaata agaacaagaa taaaatTTTT ttacaattaa ggaatatcat aacaagaatt 240  
gatttaacgt ataaataaat gccatgaata tattttccca cctaaatata cattacagat 300  
atTTTTtact atgatcagta tggtgaggac tatcgactac cacaaaaaac gctggaaagt 360  
ctatcgatga ttttacaaga tgcttcatcc ctggaaagtt ggcgcgcaat tcaaactaag 420  
agtgcaaaat atttctcaac agtcacaatc agcaaataaa ataaaaatat ctagtcgctt 480  
atattttatt atattacact taatataatc cattgattt 519

&lt;210&gt; 850

&lt;211&gt; 80

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(80))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC006247. Matches in area of ORF with sequence



549/586

similarity to mammalian Valyl tRNA genes

&lt;400&gt; 850

gactggagtc gcagaaaaac atatgaaaac gtgtgcagtt tgggaccagg gttgccaaca 60  
gatattatta ttttgaattc 80

&lt;210&gt; 851

&lt;211&gt; 370

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(370))

<223> Area matching *Drosophila* Genomic sequence

AC005129. Matches in area of 1208AA predicted  
protein.

&lt;400&gt; 851

ggtaaagtgt tgagctgtcg ctgcggctct cggcaattta tactcgcagc tcggtacttc 60  
ggctccgaac atccacttcg gcttcggcac gggcttcggc ttcgtccgct ctccaaattc 120  
ttatTTTTTT ttttattatt actgtgagtc gagtgaagct cgctcttttg tgctctttgc 180  
cacgatgact tgtgcacttg ccagtgtcc cattgtgaat gggcaacgag gggctggtgc 240  
aaacgaaccg ccacccacca ctgcacagtg ggacggatac ttaaatcatt agattcaata 300  
ttaaacagta gattaaaatt aatagttttc ccactttatg tattatagaa taagttttcc 360  
ttttgaattc 370

&lt;210&gt; 852

&lt;211&gt; 748

&lt;212&gt; DNA

550/586

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement ((1)..(748))

<223> Area matching *Drosophila* Genomic sequence

AC005894.

&lt;400&gt; 852

tgtgagtcga ggtgagccaa atacgaacca tccggaccga gccgagccaa aacgagcccc 60  
actatgccag ccgaactcat taaaaagccg agcggcattt aaggatgcgc ctgcgcagca 120  
atctcttata ctgcgcgcaa agctctgcga aaaagctccg agatcgagcc gagcttgggtg 180  
acacttttctg ttgaaatacg gcggcacact tggcacggag ctgagttact gccaaagtgg 240  
cagtgtgagt ggtgctccca gggaaggaca agccttctgg agaaggaat ggaaagcctc 300  
agccggaaat ggagccctcc agtcagacca ccaagatcat ctccggcatgg aaatggaaat 360  
ggatgtagag gtgaagggtgg tagtggaatt ggtgatggag atggagatgg cagaggaagt 420  
gagccactct agacacgaat cgtgaatcag cggcgcattc aacgtcaaca cgtaatcccc 480  
gcaaggactg actcgttctc gtcgtcctcc tcattcttcg cgaggtggag gcatcataat 540  
aatgcccccg attaaagaac aaaaagccag gctgaagtgc tgcaagtcatt ttgtgtgctc 600  
attgtgcaaa cagatccccg gtccttggtc ctgggttcctg cgccggaaac gctttaagac 660  
cccgccagcc gagggcttag tgcgggcaca taatgtctgc taatatttga aaatgcgtcg 720  
cattaattga catgaaagag tcacgaaa 748

&lt;210&gt; 853

&lt;211&gt; 535

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement ((1)..(535))

551/586

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005447. Matches in area of 239AA predicted  
protein. Sequence similarity to C.elegans gene  
AF002196.

&lt;400&gt; 853

gtgagagcca ttaaccaaga gaacagtaat agagcgcatt ctctctttcc atgacctct 60  
ttagcttcat cactctcaca tacataaaca caactttgca tatgtgtaac tttcgtat 120  
ttaacagttt caaactaaat gcatatgcc aaccaccatta gggttgaaca gaaagcatta 180  
aaagtgataa tcccataata aatgtctact tttggcagtt ttccaggaca aaccacccac 240  
tccgccatcc gccgcccagg aggcagccca gctcttgga agttccggag cggagcaagt 300  
cagcttcatg cagtcgctga agaacctgat gaccaaccgg aacttcatct tctgctcct 360  
ctcgtaaggc atcaatgtgg gcgtctttta cgccatttcc acgctcctca atccggtacg 420  
aacatacttc gcatacttcc actcgattaa tgagcggctg ctaatggggt cttattgctg 480  
ggatctgttt ccagggtggc tgaagtatta tcccggaacg aagtggacgc cggac 535

&lt;210&gt; 854

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(581))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005643. Matches in area of 242AA protein.

&lt;400&gt; 854

gcaccagcca gatgggaaac tgtgcggcag tgggtcgaag agccaatgct ctgaaaaat 60  
ctatttagtt agctattaat tatccacttg atttctaaat ataaacaatg gtgttcatta 120

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aagcagggaa gttttaatgg ggtagtagg tcagtcaagt atttattatt tagttttgtt 180  
ttttattaac tagctatgcc ttcataaata aaccaattgc aatagtttag ttattatata 240  
gattttttga tatttaatag atgtttctga ggtaggggat ccaaacgact atgettagcc 300  
atctgcaa at ccccttcacc ccatatgagg tcagtttgct gtccggcaca gctgggttatt 360  
tatttttagg catcgcaatt ggatttacia attaaatgtt tctgccccac gatttgtagc 420  
cgcaattgtg ccaactgcct atagtattcc atatgcatgt gaatgggggt tgtctatagg 480  
ccctcggggg cctctaagct tgctagcggg ggtggttccg ctataattct gggcacgtct 540  
tatgactgcc aggggtggtg aatagacat ttcattacat c 581

&lt;210&gt; 855

&lt;211&gt; 342

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(342)

<223> Area matching *Drosophila* Genomic sequence

AC005554. Matches in area of ORF with sequence  
similarity to Rat fatty acid synthase.

&lt;400&gt; 855

ggtcagaatg ttcggatcgt agtgattcat cgtggaaatc atgcgagtac cagcgagta 60  
aaactggaaa cagcagcgaa cttctccgat cgtttataag ccaattactt tgtgagaaat 120  
gcctcgcat agtatacatt tggaaaatta tcttgattga gacaatgttc tgattagtga 180  
agttcgaccg tactgaatgc gtccattatt cttaaacaat caatgcgcga ttgctacgtg 240  
tattgatagg attaggggat atgtacatta agttctacag gataattcat cagcataatc 300  
cgtacgaaac tacttccttt ccactagga cgctttccgc aa 342

&lt;210&gt; 856

&lt;211&gt; 77

553/586

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(77))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004532. matches in area of 1145AA predicted  
protein. Sequence similarity to C. elegans gene  
AF067608.

&lt;400&gt; 856

agctggccca gtggctttta ttttcgaccc gctcgcagac atcagttgca gttcggaagc 60  
ggaatcggat gatgcgg 77

&lt;210&gt; 857

&lt;211&gt; 496

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(496))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC007186. Matches in area of ORF with sequence  
similarity to Human YL gene.

&lt;400&gt; 857

gtctggctta gtacattacg tactctgggc acattgcttt agtgaaaaga aaaacgaagg 60  
tataaacttg tagaactgcc gtctaaaagt gaataattta ttgcaatcgg tgctaaaaag 120

554/586

aatgatatga gcttattaca ctgcagctaa ctaatgtaaa actcttcacg tagaagtggc 180  
cgaactgtta gccgttaatg aagttagagt tctttaggag gacgctgcca acgcgacgtc 240  
gctgcgggaa agagatggaa agcgttagcc ggcgttcgtc cgaaatttct ccgctattca 300  
actggctttt gaagcctgga gtgagcataa attaatggtc cgcaccttaa ttatcgcggt 360  
gtcgcaatta ttgtgctgtt gcagtagtgc aaagtgcgtt tcgtgcatat gtgtgccgtg 420  
tcaagtatta acgggttgtg tattccgccg ttctgcactg gtaattgggtg gcagctatag 480  
ctgcactttt ccataa 496

&lt;210&gt; 858

&lt;211&gt; 582

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(582)

<223> Area matching *Drosophila* Genomic sequence

AC007176.

&lt;400&gt; 858

gcctgtttta tttacgccga aagcttaaac acaagaggcg aaaacaaaaac cgaaacaaaa 60  
atctaaaaac gtgtttcaaa tgttcctatc tgtgttgtgt ctctgggtcc agtatttggg 120  
gtttggcgta caagcatgtg gatatggata cgaacagaac ggaaagacga aacataacat 180  
atcgaatgct atttactcca tgtgtcttgt ttcacgctcg atttgcgtcg ccagcagagc 240  
taaaaaataa aaaactacgc ttactgatta aaaaagctgt cgccggggctt tatattttgc 300  
gtcgaactga ttgtgtgcag tgattactcg gaagcgggaa ttagaaagga ccccgccag 360  
atatttattt gattaaaaaa tgcaaaagca tgctgctagc aacagaaaag aagaattgtt 420  
taaattaatc ataaaatagc actagttttt gcactagttt acactttata ctttatccta 480  
aacaccagct cgggcaacct ttttgaaaac tcgagaattt actgggtata aaataggtcc 540  
actggaccct aaacaaacag gaaggggtga acaattataa tt 582

555/586

&lt;210&gt; 859

&lt;211&gt; 483

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> Area matching *Drosophila* Genomic sequence

AC004423. Matches in area of 604AA predicted  
protein. Sequence similarity to *C. elegans* gene  
AL0214481.

&lt;400&gt; 859

gttccaacca ggcagcagta aacaaactgg atgatgccgg tgagcagaat gtagccgagg 60  
tagatgtcca ccagcttcag tcttgggcgt attctgcacg tagtcgttgt agaacttggga 120  
aatgacgctc gacagctcca ccattttgct attttatgtg atatttgtcc ggatatttaa 180  
ggataaaggc gctttttaac aaattaatcg cagacacgtc acaaattggg agagaactca 240  
aaagtaggac cgttcgtcta gtttgaaaat aatactgata gctttatcga tgaaggcgca 300  
agtacagtgg gcactcaata ccttgaagtt taataaagaa taggtttata tattaaaaaa 360  
tttttgtgtt ttagttaaaa ctaaaacata acaaatttta tagattaatg accgctatcg 420  
attctttttt aatgttgcatt atgtttgaga ggtaatggta taatttaatt tatataaaaa 480  
gaa 483

&lt;210&gt; 860

&lt;211&gt; 560

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

556/586

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(560)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005811.

&lt;400&gt; 860

```
gtctgcccc a tcttttgtgt gccggcagcg catgtgtacg tttaactttg tgtatgtgtg 60
tctctagcgg gtgtgtgtgg agctgacttc ggtgctgcgt cttcttcttc gtggtttgct 120
tcgccgccgc tgctgctcgt atggttgttg ttggtttggt caaggctggt tgcgtacaaa 180
attcaacatt atttgaaggt cgtcctttgc ttattctgcg cgctcgtttt tactcgttcg 240
ctctctcttc ccagcggggc ttttttttga atgtccctct ctgtcgtgtg ctcgattttg 300
tctttgtgca gtgcgtgggt ttttgtcttc gctaaacaca tcgaatgggt ctagtgtgtc 360
ttaaagggga aagaatttat ttaagtctt ttgatttatt agaattgggt cctggaacac 420
acttcaccgg ttattaagct accaaacatt cattggctcc aaaatgggtgc tttccaaaca 480
aagaaggggtg attcccaggg aaacataaaa ggtataaaaa aataaaagac cccaaataat 540
ttcttaaagt cccatgctga                                     560
```

&lt;210&gt; 861

&lt;211&gt; 596

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(596)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005653. Matches in area of 528AA predicted

protein. Sequence similarity to C. elegans gene

U40420.

&lt;400&gt; 861



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gttgagacaa actgataagg ataagcaaag atcactctct tgatgctctc tttgcacaat 60  
tctcaatcgt tatgatatcc tttcgatatg ccattgctta tgctgtgacc ttgaacttgg 120  
ctggacgaga cgggcacgtg acaatcaaca gttccatctt ctgcatttta aaatgcattt 180  
aagcagctct tgcagcacat ttcgcctgcc acaaagtgcg ggcagcatcg caattttgtc 240  
gcgcttgggt ttcgtgtcca cacatatata tatgtatatg catgtatgta tgtacacaaa 300  
tacataccta gcactatagt gcaactagcc ctctggttct tctttctatg tggttgctgt 360  
tgctgctttt ttcttgtggg cggttaacgc tcaagcgggt cgaacgcca tggtgcgcc 420  
cttccctgcc ctcccacctt cgccagctct ctgggttttc gcatgatgag cttgcctggc 480  
tgctgcttg gtcttgggtct tctttacacg tccttcaacg acgttcgctg gtggggggccc 540  
cgctttgctg gtgctggtgt cctggtgctg ctggtgctgt gctgggtgtg gtgggt 596

&lt;210&gt; 862

&lt;211&gt; 539

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(539)

<223> Area matching *Drosophila* Genomic sequence

AC004516. Matches in area of 17300AA predicted  
protein. Sequence similarity to *C.elegans* UNC89  
gene

&lt;400&gt; 862

atcatgcccc tcattttgtt ttaacaaaaa tttgagtaca agaagtagaa aattcgatgg 60  
tgtgctaaaa ataacattgg gccacagctg ctatcgatta tcgatatatt ctactcttg 120  
caagaatctg acaaaattag ccaagacact aatcaccact gcttggcaag cagtttaatg 180  
ggcgccaatt tcgaaatgca atatttttta ctcagtcaaa gtgctaaagc atattatctt 240  
tttttttcaa cagatatact caacaaaagc cgcattggata aagtgcacac gagacatggg 300

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taagttcaag cttattatca agatatgttg tcattaacaa gctttaacaa tttattagca 360  
acatcgagac ccttccccga ttcgttcgca acttgcgaaa tctgcgctgt tgcgatgggg 420  
atgcatatc gctggaatgt cacgttgagg cccgatccgg agcccgttca tcctctggga 480  
aaaggatggg catgttgtgc ccagcgatcg ggactacgtg atgtccttcg atgggacca 539

&lt;210&gt; 863

&lt;211&gt; 505

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(505))

<223> Area matching *Drosophila* Genomic sequence

AC005285. Matches in area of gene with sequence

similarity to guanine nucleotide exchange genes.

&lt;400&gt; 863

agctgaaaac taaaagtccg acgcgtctta cagtgtgacc acaccgctca gtgataccag 60  
gttttctata ctatctatga ctatcgctga attgcggtat ttaaataccg attgggttgg 120  
atagattggt cactaagttc ctttttaata cgctagtggc gccactgctg tttcaaaaaa 180  
taccegctga tctgggaatc ggttatttct gctttatggt ttttaaaaca tttatttata 240  
gatggcgctt tgggtgatttt tattattttc atacattacc gttatcaatt tataaattgc 300  
aaacttttta aaacaaagtc aagtttgccc cagaaaatcg aaatgctgtg tttttaagga 360  
tttttcttta tttataatct aatggcaatt tcttccattt caaaaagcgt acaattctga 420  
gtttcatctt tagaggctct ttataactgg gcaatgtgct caacgatttc tttcttgctc 480  
tacttttggc ttattatatt ttgag 505

&lt;210&gt; 864

&lt;211&gt; 504

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(504))

<223> Area matching *Drosophila* Genomic sequence

AC007137.

<400> 864

```
cgcggatcgc tcggctggcg gccctcatt tacggtcga aactcgtcta ggccagagca 60
tctttgcatg tgttcgtgat tctgtgtgag cacgttcgct ggatcgtctt acattaagaa 120
agaagtgtat tagcttcgat ttattgcatc gttgcctagg cccctgcttc tgcctcggtc 180
gctgcctctg ctggcgctgc tgatgcagtt ggcgtcgtg tcgacgtgtt ggattgtgag 240
tctcgcgtgg aagtgggaat catcactggt ggatcgggga tcggtctttt atcgttgtgt 300
attcattcag agcaccata cactcgccga agacgtcgtc tatcttgctt tttttccttc 360
tgttatgttt ctgagctgag ctgctgctct tttcttagct tttcgttatt aggaaatcga 420
aaactgaagc tgcgactgcg actgggggtct atcatcagtc ccgtgagacg gtctcaaact 480
attggtcgtg gtggcgcttt ttgc                                     504
```

<210> 865

<211> 191

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(191))

<223> Area matching *Drosophila* Genomic sequence

AC005643.

560/586

&lt;400&gt; 865

gtgcgagcgc ccttttgaga aaaaccaagc gaaaaaagtt aaatcgatag cgaaccgcgc 60  
cactgaagcg ggattatcta acacggctta cagtcggtt cgcccagaat cgcgacttta 120  
ctttccactc tttgcacttg tctcgatttt tccagctacc tttgcgctcg ctaaaaaaaa 180  
ctctcgaatt c 191

&lt;210&gt; 866

&lt;211&gt; 468

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(468)

<223> Area matching *Drosophila* Genomic sequence

AC004642. Matches in area of gene with sequence  
similarity to mouse lysophosphatidic acid  
acyltransferase gene.

&lt;400&gt; 866

caggagacgg aacggcttct tgttccactg ccaatcggtt tgaaagggtt gaatgaacgt 60  
gcactgaaaa caaaaggcac atttacattc agattatatt gttattgggt atgtgttttt 120  
gacagacctt tgcttgcact tattacttaa atcaacaagg cacatttaca atcagtttat 180  
attgttattg ggtgtgtttt tgacagacct ttgctgtac ttattttcac taaacaaaat 240  
gttataaacc aataaataat aattgttagt ctaataattt atagtctgat attatggaac 300  
acaagtgtgt gggctatata cacaccataa ttaatatct actttgggtt gtgccttatt 360  
aattacaaaa tatagaataa atcttttagct atagctaaag ggaaatcgac aaaagtcgta 420  
tcggtttgcg gaatacccct gggcattccg caagtgcagc cacgaaac 468

&lt;210&gt; 867

&lt;211&gt; 578

561/586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(578))

<223> Area matching *Drosophila* Genomic sequence

AC005749. Matches in area of 1481AA predicted  
protein. Sequence similarity to Human KIAA0596  
gene.

&lt;400&gt; 867

ctctgggggtg gaccttggtg gtaagctcat gtttgaaacc atgtaagggg tcaagtttac 60  
tgtatacccg tgcccagtgcc cccaaaaaat atgtcggttaa tttaacgttt agctttaagg 120  
aaagttcacc cttagctgga cttttggggg ggtggctgcc caactgattg tgtcccatat 180  
gttgcccgat tacgtcacct gctgcgcggg cttttcttcg taggctgtaa taaacaccga 240  
ttgccaaggc aattttaaac gatccgtaat tgactcacac accggggtttt ccgaacttta 300  
tttttgttca gtaaagtgtg aattatgctt tattacatgg ctttcaatat ttcttaggtg 360  
taacaatata caattcctgc agttagtcgt tttagtcgct tatagatgag gatattattt 420  
ggttctgaat gaagtccatc ccatacatat atatattata tagggttgga gtcttggtat 480  
cctggggcat atgacgttgc atatgtgcag gactctgaag gttagatttc ttgacccaaa 540  
tctttgcgca acagaaaagt gaagccttag tcatgggc 578

&lt;210&gt; 868

&lt;211&gt; 598

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

562/586

&lt;222&gt; Complement ((1)..(598))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC007185.

&lt;400&gt; 868

atTTTgcctt tctgtctgtc tgggttgtgg cgctagaac tttccatcaa aatgctgcga 60  
caaagcaaat gggccccaac attttggaaa acccgaataa caatatgtc tattttttac 120  
gaaattactt ttctatcggtt atatggtatg tccacatgta tttaaacaca tagctgtcaa 180  
aagtgtcgat ctaagacttc cgacattgcc tattgaaaat taaaatgtat gattttgtac 240  
atatttttct ttttccattt tcgatttcca ttattttccg tcaaacgcct acaaagtca 300  
aaaatcgaat gttgcctatt ggggcatccc gagaataaga gttcaacctg gggtgtttat 360  
ttttgttg ccccgctgct gtttttaagt ttctcaact acgccgccca atccccctc 420  
cactatcact ccgccgtat cgccatctct ttccgctgc ttggtgctat tgggtggtgca 480  
gctgcttttg gtggttacgc attcggagca aaatggtgcc tgcgtgtgtg tgtgtgtggt 540  
gaaatgagtg cgctgtgtgc ctgtttgcat ggctggataa taatttggtg aggcaaat 598

&lt;210&gt; 869

&lt;211&gt; 634

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(634)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004340. Matches in area of predicted gene with  
sequence similarity to human sec24 homologue.

&lt;400&gt; 869

tttcgagcta aacgaacttc cagtcagtt ccctaattcg atcttttttg ctctttttgc 60  
cttgccacgt aagctatcgg taatcggcag tggaaaatcg aatgtcaatc gattgtgctc 120

tttcggctgc catcgccgaa tcgataatcg tgttgaactt aacagcgctg ctgttagcga 180  
acagctgcga gttatgttat gtgtaaggtg gtgcaataga atgcagtgc gtcattaaat 240  
acgttgggtt aaaataaata agtgaataag atataatcaa agtacattta aaataaatat 300  
gtatatatttc acaattttat caaaatattc cttacattca ggggtttata ttaaatttaa 360  
tttctggctg ggaggaaatg ttaccaaagg ctcagaaatt tcctccaacc tgccggccca 420  
agccctgggt gtccaccgta aatgaagtcc ttccgaatt ggactaccgg gttgcatgat 480  
cttggtaaat ccgcagtcct gtgtaacgct ctatttcgct actttgacct gtgggcattc 540  
aacttgccgc cacccttcgg ctggtttcga tgataaagct tcatgaaagg ttggggatcc 600  
cggaacttca ctctcacgat aatccttaaa gaaa 634

<210> 870

<211> 415

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> Complement((1)..(415))

<223> Area matching *Drosophila* Genomic sequence AC5456.

Matches in area of gene with sequence similarity  
to Human GMP synthase.

<400> 870

tttcggcttt aattcgcgaa aaaactgcag gaaatccaaa aggaaagtcc ctggaagcgg 60  
ccataataac gcagccgtga aaaccacagg gatttcacgc ccagctgtgt cgagcagccc 120  
tggtactcgc gaaaagaagc tgcagcagcc gaagaaattt tgagtgtgtg cgtgaggaag 180  
gaaaacgggg gaccgcaaac aacggatcgc gaatttcgct ttaagacaaa gtcttgcgct 240  
gcttgtcacg gtattccacg gccttgccga cggacttccc ggttctggaa aaccgcagcc 300  
aggctaaaac gagagaaggt gagagtcgca atatggcgaa aaagatcccc gatcccagcc 360  
aaatcgccat gcggtgctgc tccgccaca attccgaacc ccgcccgttg aattc 415

564/586

&lt;210&gt; 871

&lt;211&gt; 198

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (198)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004375.

&lt;400&gt; 871

attccagga tacagatata cacagacaca cacaatacac tggcacacag gggcacccga 60  
ttccgccgtt tgttttgcgg ctaattgttt atacagcgca gattattctt cgcactggat 120  
gtatttgttc atccggctat tttcgtttgt ttttgctccg cagcagcaaa tttgcagcgc 180  
acacgcagcc gagaattc 198

&lt;210&gt; 872

&lt;211&gt; 316

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (316)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene matching Human

NAT1/death associated protein.

&lt;400&gt; 872



565/586

agtgaatca ataaaagtga ggagctcccc tagatgccat agtcgctcca tcgcggtaat 60  
aattttcaag agcaagcagg gtcgaaattc gtcaatcaaa acgttaattt gcatgaatca 120  
tttcgagaga aaaaaaaca caaagaaagt ttacgcgtat gactgtgtgt gtaggtaca 180  
cctatttgcg ccacaaaatg gcgtcggcac cgtcggaaaa tctgaaatgc tgtgtttgga 240  
ccgttgcccc ctgcctttgc ttggagttat ctacagtgcc cctcccccg gggaaagaca 300  
gccctctcat tgggaa 316

&lt;210&gt; 873

&lt;211&gt; 495

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(495))

<223> Area matching *Drosophila* Genomic sequence

AC004154. Matches in area of human rabt

geranylgeranyl transferase.

&lt;400&gt; 873

agtgaatcca atcgagcaca gctgattcat ttgcgcgatg gttggcaacg cggcagtggc 60  
ttatcaaaca gctgatcgac gcaggggtgt agtgtaggg ggttactata accccatcca 120  
aaaataaaaa ttaaacttac ttaaatttca aatagctagt ttattttatt caaaacacat 180  
gcacactatt gcaccagcag gctggactgc ggatccggct cgtcgatgct tagggagact 240  
atgtgctggc cgggaaccat gacgttgccc agcaggcgcg gtcctgggcc ctccaccaag 300  
tactcggcgc acatggacag cacgatgttg gcgtcgcggt ccgtgcagtt gaagaatccc 360  
accagcacgc gtccgtccgt aatcacgac cgcagaactc gaccagccac ttctggagct 420  
tcctgcgtcc cggcgtcaaa ctggcatcgt catctggtgc ggggccgtcg ttgtgatgcg 480  
gaaggctccg ggggt 495

566/586

&lt;210&gt; 874

&lt;211&gt; 116

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(116))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004328. Matches in area of gene with sequence  
similarity to Mouse BOP1.

&lt;400&gt; 874

agtggggcga agagtcccga gctttattct ctttttccga ctgcgcaca tgtcttaccg 60  
tccgttctct cgcgtctctc gctgtcagt ccctctctg tgtgtaccag gaattc 116

&lt;210&gt; 875

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(581))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005112. Matches in area of 407AA predicted  
protein.

&lt;400&gt; 875

gtgcgctctt tttcgcagcg agtttcgtgt tctggtttta ttttctctga ttctgattgc 60  
gattgtgaat ctggttctgt gtgaatttcg tttttattaa taaaatgcac aacttccgtt 120

567/586

attaattttg caacgacaac aattgctgcg tgtgtgtgtg tgtgagtgtt tgtgtgtttg 180  
tttgcggtatt tgtgacagcc gctgacaggc gaaaagcaaa agcaacaaag tgacaagcat 240  
gagcgtgtgt cgcctaggag gaaaagcgga aaagcagacc gaaaaataat aacaacaaaa 300  
agtgggcgac aaacgggagg tgggaggcaa tgaacggta caacctgtcc gcttttttac 360  
cacgccccca cttccccgt tttcttcaac gatttcgtc ctgtgcacgc gactcgcgt 420  
atctcgtct ttnngtgagg ttttttttc tgetgntagc tgattcattc ataaaaatcg 480  
ggttgtaaaa aaagaacagc ggnacagaaa aaacgcgctg atttatttat tatgccattg 540  
ccgacgcgtc gcgctgagtc tgggntata gttccctaga c 581

&lt;210&gt; 876

&lt;211&gt; 506

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(506))

<223> Area matching *Drosophila* Genomic sequence

AC004367. Matches in area of 387AA predicted  
protein.

&lt;400&gt; 876

ttctcatat tctgggtatt tctcctaata cgaatataaa atctatctac tggcacacta 60  
ggtgaggaaa ttatggacca caaaagatta cttcatatgt gcagttagag tagtagaaac 120  
catccgtcat taacaaaaag aacttaaatt taaaacgtta ttattttatg tatctgtata 180  
catatatggc taaacttgat taagtcttga catggaaggc atttttggca gtgcggagac 240  
acagcacttg atcaaagtgt atagctccca atgtggcatc cacagttggg acagtagtgc 300  
tggacactct tgcagttagt gatgaagtag ggaaggcaga tgaaggcca gcagctggag 360  
aatcagggtta gcaaagttag taagcccgtt ggtatcctga cgccccactc accagcagat 420  
ataccaggtc agacgcacat gtgggtcttg ccggtggggg acgtggcaga ctggtggtga 480

568/586

cctcgccctg caggacggac acttac

506

&lt;210&gt; 877

&lt;211&gt; 411

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (411)

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005472. Matches in area of gene with sequence

similarity to Human NAT1/ death associated

protein.

&lt;400&gt; 877

gtgtgtgctt tcgtcactat cgatggggga aaaagaagag tgcgttttca tgggttttct 60  
caagatattt gctcttgaag ccccgaaaaa ctagtaaaat aaatactgtt tgcaatgtgg 120  
gtgtgccact tggccagtta aacatgcaga cagcgacaaa cacttgtgca caagagccga 180  
gccgaacgct cgaattgagg tcaaaatcat ccacaactgg gtctgtgcgg aagcaggggg 240  
ggctcatttc tcaggtcggg gtcgacgcct caatgcagca gaggggtggg ttttcgcatt 300  
gggggggtgg taagttttgg cttatccctt ccccgcacga aagactacat tattgcaggc 360  
ccaaagtctg tatgtatgga tgtggtggta ctcgcacaat gacaaatcgc a 411

&lt;210&gt; 878

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

569/586

&lt;222&gt; (1)..(492)

&lt;223&gt; Area matching Drosophila genomic sequence AC007121

(41693-21184). intron of gene at

22511-56594bp(complement) coding for 365AA

protein.

&lt;400&gt; 878

atgtaaataa ttataataga aagaccgaac tatgtcagta gtgtgtatgc acaaatgttg 60  
ctcaaaataa agcgaaaaaa ttgtgaaata ttttcgtata aaaataactca caccgcaccg 120  
agtctgattc tattcttgat taaaaacaaa aagtgaaaag agagtggaac agagagagag 180  
agagtgcaga caaatggaag aaacaaacaa aacgcagaga aaaaaattac caaatattcc 240  
gagaatactt ggcattaagc aatcgccaaa agactgggcc gaggggaaga gatcgcccttg 300  
gaactagggg ctccaatgcc gaccaactaa cacactggcc agccctggtc tgcaaccatc 360  
tctatctcgc ccgccgtcca attagtgcag cattcttaaa gcggccgagg caactttctt 420  
ctactcccca aacgagtttc agccacgcac caacacacca acaccaatac cagcaacaac 480  
atgacggatg gg 492

&lt;210&gt; 879

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(291)

&lt;223&gt; Area matching Drosophila Genomic sequence L49405.

Matches in area of 626AA predicted protein.

Sequence similarity to human NAT1/death associated  
protein.

570/586

&lt;400&gt; 879

gccactgcaa taatggcccc aaacgacgat gccaatcgt gacgccagtg acttcggctt 60  
tcggccgcct ttcgggtttt cgaaattcat ccgtttcaga gaaggaatga actctcggtg 120  
ccggagagtt gttcactgga aagtcctact actataagct atttactctt ctcttacgct 180  
taagattata tggattatta acatctcatt atgcgttgaa ccaataagtg tgttatatct 240  
tcattaaatt aaatattatg tttaaaatca aataattgcg tgatttaata c 291

&lt;210&gt; 880

&lt;211&gt; 454

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(454)

<223> Area matching *Drosophila* Genomic sequence

AC004658. Matches in area of 394AA predicted  
protein.

&lt;400&gt; 880

gttcccgtta tctgatccag acatataggt ctaaagcgct ctccggggcgc tgcctagagc 60  
gcgactcgcc ggatggaaac cccgtttaat cgcaatcaca agccacagaa agtaaaagca 120  
agcgaaaagc ggcgtcgcac acacacacac acacaacagg gagtaacgcg cagaacgaaa 180  
caacagaaaa tgtgtgtaat acaaaaatcc gttgacgcgt tcgcatttgg ttttagcaga 240  
ggaattgtcg agcgttcgta cgtacttgca tacatatggt atgttatggt actacatgaa 300  
tgttaccata tacacatggt atgttacata catacatagc ttaccaaata acttggtatg 360  
cgtttccttg gcagaaatac gcctgcactt cggccatatc agcttcaatt aatatagggg 420  
gttcaatccc cgtatcgga caatttcgaa gaat 454

&lt;210&gt; 881

&lt;211&gt; 376

571/586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(376)

&lt;223&gt; Area matching drosophila genomic sequence AC007757

( 38974-39348bp). This sequence also matches

*Drosophila* EST AA951801 which has sequence

similarity to transcription factors.

&lt;400&gt; 881

ggttagggtgta aaattaaagc cgaatattat caatccatt ccaaagttca attttgtgtc 60  
ggaaccatag taaattaatt gttccttgct attaacaacg aaaaatgcat atttagctat 120  
tgcagttgag acggcagcta ttgcttcttc accacgctgg gaagttgaga atcgcagaca 180  
aataaatctt cctcctcctt cgtccggtcc gaccatcaac ttcgatttca atttcataca 240  
tttcgtttgc gtgggacaag cgagcgacag cagtctctgg agttagcgga tttatattgt 300  
ctcgatttgc tgctgctggt gatatttgatg atgtgttgc tgctgtctgt tgttctccgt 360  
aggggtgatt gactga 376

&lt;210&gt; 882

&lt;211&gt; 597

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(597))

<223> Area matching *Drosophila* Genomic sequence

AC006091. Matches in area of 564AA predicted

572/586

protein. Sequence similarity to yeast YII3  
hypothetical protein.

&lt;400&gt; 882

accagacaa tacgaatttg ttttgetgcc accgctgcat tatcagtaga caatgaattt 60  
ggggttacgc tttctggcaa acaaagtaaa agcgtgttgt ggctcaaaaa agcagcatta 120  
attagcacag acgaggtcaa tgaaatagca atgatggcgt caataaaata tatgtaaata 180  
ttttaatata tttattttaa ttggaataag taaatagcag cctgttttac tttccgaaac 240  
tcaataacta actttaacca ttccattcct actttaatca ctgccactgt acactttaag 300  
atgtgtttga atacgtatgg tttttttttt tgcaaacctg tccgtttata catacatata 360  
tactatatag cagaactgaa acaataaaca catttctaata gccacaaacg aatcgccaat 420  
gccgatcgct tttgggattc gcataaacgc ctcacgaatc gcgtcaaaat cgcgcgtag 480  
ctggtggagc ttccaaaaat tcccccaaac caaaagccaa tttaaattcg aaaaagccat 540  
gatttagcct gatgtcttgc aatttatgcc ttcgacattc gttagtcccc cattttg 597

&lt;210&gt; 883

&lt;211&gt; 498

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(498))

<223> Area matching *Drosophila* Genomic sequence

AC005720.

&lt;400&gt; 883

ctgcagacga agcgccgaag cagcgtcggt tgacgtttct tttcacatt ctctcacttt 60  
tgctaagact ctcacgtgg cggtgcggg tgacaaaggc tcctttaact attccactat 120  
gctcaagttt ctggttaagt ttccggtttc ctgattcaca cctgaaaatt actacactcg 180  
cctaagtata cggtatgcat atcagatagc agatacaact tttctgtggt ttttgtggt 240



573/586

gtgttgcttt tcgcggcgat gacgcgcccc tgcacagtgg tgaaatgtgt tgtctagggg 300  
ttcaaaatca aaaccaatta tttgattaaa tattaatgat taatataaat gacaaaataa 360  
aatacatttg aaaatacctt cccaatatct aacttcaca aataaaaaaa tagttattaa 420  
aagttttaag caaaattcca aaatattctt gctcggataa aacaagagtt ggatggtaaa 480  
cggtagaagt gcgccaaa 498

&lt;210&gt; 884

&lt;211&gt; 375

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1) .. (375)

<223> Area matching *Drosophila* Genomic sequence

AC005814. Matches in area of gene with sequence

similarity to Rat NAB1 transcriptional repressor.

&lt;400&gt; 884

tgaggaacct tttggaaccg gccgacgaca gcgaagccaa cgaagccacc cgaagtccac 60  
ccgatccggg cgctttcgtc tatcagccgg ggcaaaaaaa aaaggggtta aatcagggat 120  
aaaaacaaaa ccaaacaat tgttcggagg gttagggacg taggacattg gtttccagat 180  
ttgaggggta ctttttatct gccgatgctc aagattctct tattagagaa caatcgggtct 240  
ctctctctct tcgcaattga gcgactttga gtgagttttt gtgctccgcc tcttgagaag 300  
cactcaaaga tttggaatgt cttgggtgcc ggagagactt tccaaatgat ccttttaatg 360  
tttttttttg gtgaa 375

&lt;210&gt; 885

&lt;211&gt; 486

&lt;212&gt; DNA

574/586

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(486)

<223> Area matching *Drosophila* Genomic sequence

AC004713. Matches in area of gene with sequence  
similarity to CD36 genes.

&lt;400&gt; 885

tgccgtactt tctgtgcttg tgccctctct ctgcccttcc gctctctcca ctcttccttc 60  
cgctctcttt tcacaacaat aaacaacaac aaacacgcgg aatgcgggat gagagccact 120  
ttttagttgt tgtagtcaa ttgtttgcct attgaggaaa agcgcgcaat caatatcaat 180  
tcgccaggcg tgcttgaata atttctcttc ttatttattt tttctttgtg aatagggggg 240  
tgtgtggtta aacaacaaac accaaccgtt agcgtcatca ccgcacaacg cacatttcac 300  
gagtgaatc aaaatcaaat gcgaaatgag cacaggctga aagcagcgac gtccgcagcg 360  
cagtggctgc gcaagtttcg ctttttgccc agtctccatt ctctcttctt tctggctctt 420  
cgcttcttga ttcttggat ttttccttgc gcgctctggt ttggtgcat tttttcgtgt 480  
cttttc 486

&lt;210&gt; 886

&lt;211&gt; 544

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(544)

<223> Area matching *Drosophila* Genomic sequence

AC005813.

575/586

&lt;400&gt; 886

acaaaccttg gttaatcggg aacattgctt acattaagcg gtgtaagaga gcagcactta 60  
gagaattgta cactctttat cttgctcaat tgaactttga agagagccgg caactttgtt 120  
tggtgcgacg ccaaatttca atgtcgacgt cgcagtcggc agcgtaagct ttcgagcagc 180  
gaaaacaaca aacggatgcg agtaaagcaa aagagacaca aaaatgcagt tgtgaatcta 240  
gtactaagat taaattatta cagacaaacg taactttatt tgcactagaa aatattacat 300  
attatattat tatcttgtgt atatatatat aatacttacc gaacaccaag tactttacag 360  
tattcaagta tttcctttta acgtaattaa tgaaatatc attatcttta atcttaattt 420  
aatataact aaacttcac tcaaataagga aggcgcggat taaaatcgga atagagatgg 480  
caaataaacg aatgggtgtgc ttactaaag gtgagttgcg cagttgctag tagtgtgacc 540  
agac 544

&lt;210&gt; 887

&lt;211&gt; 549

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(549)

<223> Area matching *Drosophila* Genomic sequence

AC006936.

&lt;400&gt; 887

cgtagctct tccgtcagc gaacccatcg ctggcacgcc cctcaacctg cagccaatga 60  
gtgaaatctg cggcactcaa ttctattcaa catggccgcc aaacggaagt cactcgaaga 120  
gcgagagagc gcgttggtgt gcaagtgtaa atgtgtgtgc gtggctttcc cctgctgtgt 180  
tggtcgtttt gcagactttt tgcaccttta ttgtcattt gtgtgtaatt tcggaaaatg 240  
ttggcacatt atgacgctcg acgccagttg ggccggggtc gcgcgcttaa gtgtcctcca 300  
gggtacttac ttcgtagca gaagtttctc gccctcatcg tccttcgtcc tttgcggggt 360

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ccttggtgct gtggtttggt gctgtgctgt ggctgttgcc gtgcggtgcc gcaactgtgtc 420  
gtttgcggat gtgtctctta ttttcataac tgtaaattgc tttagatatt aagtctgctg 480  
tactagctgt ggatttccaa acggcactgt atgtgtgcgt gtgacagcaa aaggacgaag 540  
gatgggtct 549

&lt;210&gt; 888

&lt;211&gt; 306

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(306))

<223> Area matching *Drosophila* Genomic sequence

AC005425.

&lt;400&gt; 888

agccagagag aacttgacag agctgcatcc ggcgcgaaca aatcgaaccg gttatgtcag 60  
atagaaattt taaaaatttc ttgtaaataa ataaaaatcg aagtatctgt aaacatatac 120  
attgaaatta cctgagctct agtaacaact ctttaaaaag tagagaacct tacaattgga 180  
atatataacg aaatacacac attttgcgga aatgtatggc tttctttcag tttcagcttt 240  
gtttgccctc ctttttttta atttcaccag gttctcaaaa caagtttacc atcgtgcaaa 300  
gaattc 306

&lt;210&gt; 889

&lt;211&gt; 579

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

577/586

&lt;222&gt; Complement((1)..(579))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC005720. Matches in area of 394AA predicted  
protein.

&lt;400&gt; 889

cccacgacca ttagccagcc gcatcgcccg cgtcccggcc aaggggttgc tgagaccag 60  
agtcgggggtc tggacgcctc ttccaggctg ccctggccca catgctttcg tcgttcagtc 120  
ctctcttaat ggggggctct cgtaccctca ccctcacaca cagaggcca cttgggtgtg 180  
aaagttctgc tgggctctgt ctgtgtcacg cttatgattt aataagcaaa tgtgctgcga 240  
aattgctgaa attgtttggc tgcctgcat cccacaatc cgaatctgc cccacgccct 300  
gaaatcactg tccgccgtat ttcgcattga aatgctttag ccaatgcgtc acggaagaag 360  
aaaagtgggc ggtagtccgt gcttgccctt tgattctcgt acctttaaat gcctttgcat 420  
ggagctagtt cttgcctaataaatcataat aaaaagttct aggtctgcaa aaatctaaaa 480  
tctcattcgg accattggaa tatttaatta tggtattatt atattaatat tcatagattg 540  
tttccaagtg caggtgatag agatttagaa aacgaattc 579

&lt;210&gt; 890

&lt;211&gt; 191

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(191))

&lt;223&gt; Area matching Drosophila Genomic sequence

AC004266. Matches in area of 931AA predicted  
protein. Sequence similarity to C. elegans Zinc  
finger gene. Drosophila EST AI259457 comes from  
this gene.

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&lt;400&gt; 890

gctcaaagtg agagacaggg agagagagag agtacacggc gtatgtgaaa gattcacttt 60  
tacacatcca aaaaagagat gtgagttatt ttaaattgtag tattaaatta atctgaattt 120  
ttgccatatt aggcaattat ttgatatcat tttttgatca tgatcttttg taaatattct 180  
ttttggaatt c 191

&lt;210&gt; 891

&lt;211&gt; 264

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(264))

<223> Area matching *Drosophila* Genomic sequence

AC006936.

&lt;400&gt; 891

ggaaagaccc cgaccacac tcgtgtggcg cccataaaaa cgatcatcgtt gcacataaaa 60  
cccgacagca aacaatgcag cttgccattt ggctgccgcc gtaatagttc tttaattgct 120  
cacaaaagtc gtcaaagttc gactcctcca cccatataca taaatgtata ttaccacaa 180  
gcataaacccg tacaaggtaa agtcggttgc tcgttgctcg tttgggcca ttaatcactt 240  
ggagtgtagg gaggaggctg gggg 264

&lt;210&gt; 892

&lt;211&gt; 537

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

579/586

&lt;221&gt; misc\_feature

&lt;222&gt; (488)..(536)

<223> Area matching Drosophils EST AI062190. This EST  
comes from the Drosophila ferrochelata gene.

&lt;400&gt; 892

ggccgcgcct tttattgcgt ttttacgaag caattgtgcc tgcattcggg ggaaaaacta 60  
caaaatatta ttgatcgga ggaaacgaaa cactcgcagc aagcgacgag agcgaaatgc 120  
agcgtgcaag agcgagactg caccacagtc agcttttacc gttgcacgca gcgttgatga 180  
caagggaaaag aaataaggac gcatgcgcga aaaatttctg ttggtcgctt gaagaacagt 240  
atatacaaaa tattggtttc ggtttcaata aagagaaatt aaatggtaaa tgtgtaacaa 300  
aaggaaaaat ttttaaataat ttagattact gttgagtaat agttggcagc tattttacac 360  
acatagatgg cgtgacggtt actttttaca gaactctggt acgtttggaa aaatcagatc 420  
tgtgagatca tacattttgg tatttaaact attttagcaa ctggtaacac tattcgacac 480  
cggtgccatc aattttgggt caatttaaaa ggaactatgg ttttgcatac acaaagt 537

&lt;210&gt; 893

&lt;211&gt; 1068

&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((4)..(579))

<223> AF104256. Area showing translational sequence similarity to  
human CRSP150 transcriptional co-activator  
protein.

&lt;400&gt; 893

actgggcaca atgggaaccg ccgagggcgg catgcgcaaa catatctgca ccgtccattt 60

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caactggtcg ccaccagct ccggttcaa atccaaacgc atgatctgta cgaaatcctt 120  
aagtacctgg gcgggcaggt tcaacagccg gcagatgctg tgcagggaat tgggtcggta 180  
tggtggagct gccactctgg tgtcaaagta ctgctctata accagcagat cgtcctggct 240  
aagctggaac ggcggcggat gcttgtcggg catgggcggc agctgagaga ctttgaggtg 300  
cagcgtctgc atgtgcatct gattcagcac cacctggcac tgcagtccat cgaccttgaa 360  
gagcaccact cctggttctg tactgtttag ggcggtaagc gtctcctcgc tctgaatgtt 420  
tctgtgcaat tgccttctca tataaacgca gcctagaaaa cgctctagag gactcatgtc 480  
cggcacattg atatccttgt tcggatacgg actgggacga cacagagtct ccaaagcttc 540  
atgggtgagg agagtaggaa ctgctccagc ccagggccga ttgagagtgc ctcgagagcc 600  
tcctctatcc gtgccaccgg ccactcctgc tccaccaccg gtgctcttgt gatcaggact 660  
ctgtccgggt cgtggagatg ggcgcggcat gctgggggat ccgggccaat tgttattcgc 720  
cggcgacatg gcggtgaagg gagagtcttg gtggtctctgc atgtagagcg tgttggggtcc 780  
aggactatgg accatgtggg gactgggctg aggatttagc ggagacgacg gcatcaagcc 840  
gcttgggcgc ggatgtggca tatgtggcgc tggcggtgac gtcaggttga agttgcccg 900  
gtccctgggg tccactgccg ccacctgccc ccgcacttgg atgccgactg gcgggtgtgt 960  
gcggatttga actggaaggc ggagtgtggg gggcaggaaa acgcagccac tgctctcggc 1020  
gattgcggtc ccgcatttca gtacccaaaa tgggtgaggat ccaccaca 1068

&lt;210&gt; 894

&lt;211&gt; 597

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (101)..(597)

<223> Area matching *Drosophila* EST AI388606. This EST  
forms a 1294bp contig with ESTs AI258281 and  
AI258326.

&lt;400&gt; 894



gctgtggctg tagtcaagcg agcgcacatg agtcagattc gtagcttttg ttttgttcag 60  
tcgagtgcga gttcttggcg attcagatac tcgctgccat ccgaaccgaa ctgaagtcca 120  
agtcgaatct aatgtgcgta cttacgtgta gaacagttca agaaaatgtg cagacattca 180  
acggtcgcat ttgtgtggat gtgtggttgt agtgaagagt gccagcatta atcgcatTTT 240  
tcccctgcac gagcaccacg actagaaaat actcgacacg tctgtctgtt tttctgcttt 300  
attgcttcta cgctattctg cttttccgtt tcggttttcc tccgcttggc ctagtgaaaa 360  
acaacaaatt tgattatatt gtgtaagtta tgtctagcat tgaaaagatg aaaagtgtca 420  
ttcctataaa tacaccacca cctcgggaaa ggcactcgca atagagaaac tggccaaaac 480  
ccaacaacaa acataacaaa caaaggaacc gcttgaatat aaccaactt tcggagtaag 540  
gggctgacta aaaaggtatt agtgcgcaac catcatgact aactcaccac ccaaaac 597

<210> 895

<211> 491

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(491)

<223> Area matching *Drosophila* genomic sequence L49408

(58018-58506). No good predicted exons in this  
area.

<400> 895

gttgagcgcg acagtgggag agagaagagc gcgcaaaagt acagatgccg ccacacacac 60  
atTTTTtact accacacacg tttcattgaa aaaacatata cacaaaagct aaggccgtaa 120  
accactgca aatttgcgaa aaaaaaacg aatgaaatg aaaactaata ccaacacatg 180  
gcttaaaatc tgctgcgcaa atTTTTgggc gatggctctg tgtgtttcgt tccgtatgcc 240  
aaaacgtttc gcttgTTTTc gtttcatttc cacaccgctt tTTTTTTTTT tTTTTgtctt 300  
tttcccatgc ggcatttatt ggcaacctgc gagcaaaaga gagggcgact aggggttgtg 360

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tgcaagggga gatggagcgc tacggcttgt ttatgaaaaa cacatgattt tttgtgtcca 420  
acagtttttg ggggcatggg cgaagagagg aagcacagga gtgcgaaaac tactattccc 480  
catagtttac a 491

&lt;210&gt; 896

&lt;211&gt; 475

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; Complement((1)..(475))

<223> Area matching *Drosophila* genomic sequence AC005714

(161048-161518). In space before gene at

162294-163466bp coding for 390AA protein similar

to human death associated protein 3.

&lt;400&gt; 896

gtccatccaa ggaatacggg gtttcggcac ctatgccgac gatcttcaga gtataaagtt 60  
ttcctcgccg gttaccctga ttctgggcga gaacgggatgc ggaaagacga ccgtggtaga 120  
gtgtctcaag tacgccttga ccggcgagtg tccgccgggc agtgatcggg gcaagagttt 180  
cgtccatgac cctaagatct ttgggctaaa cgaggtgcta gcgcagatca agatgcaggt 240  
gcgggacagg ccgtggtgcc caagtgtcca tctgccgcac catgaaggtg tccaagaagc 300  
gcaacaaaat gtcctttgaa acaatggact ccaccatcaa cttcctgacc ggcgctggac 360  
agtcgaagcg cgaaaagcag gactctctaa gcggccgctc cgtggatatt cgacgtggcc 420  
atctcggact tcatgggggtg tctccaggct attatcaaca atgggtcctgg ttttg 475

&lt;210&gt; 897

&lt;211&gt; 461

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

<220>

<221> misc\_feature

<222> (1)..(461)

<223> Area matching Drosophila genomic sequence AC004375  
(31191-31647). No good predicted exons in this  
area.

<400> 897

```
cgttcaacca tccacagtgc tgcgactat cgattgtttg tgttcgacta agatategga 60
gtggaatgtg tttggtttaa gtgtgggcat aaatcgatca atcgatcaac ttctatttta 120
gtacatatcc aaattcaaac tcttcggtta acgatctaaa cggaaattta tcttgccctgc 180
ttcttttaat aagtataatc ttgaatatat tggcttgaag ttttcataag aaacactttt 240
atttaaaaaac attttggcta aatttcagcg cctaaattat catcgatatt cgccgccaca 300
ccccaagggc agttctccca atggccctca aacctaaact ggtgtttccg atgcaggcag 360
ctcctccagc ttcagctgac ttgcgcagaa tgaactgggt ccgtttaccg tgtcgcacca 420
gaagaaaggt atccccagtg aagtcctttt gactcctctg g                               461
```

<210> 898

<211> 507

<212> DNA

<213> Drosophila melanogaster

<220>

<221> misc\_feature

<222> (12)..(419)

<223> AF000177. Area showing translational sequence similarity to  
human CaSm protein.

<400> 898

584/586

gcatggacga cttaaatecg ctggcgggca cggctcacct cctggaagag gttgacagt 60  
agtaaatecg aatgaaagga aggccagtcg ttaaaaaccg gcgcattgca gagaaactga 120  
tggtactttt gagagacgga cggactctga ttggatacct gcggtcctg gaccagttcg 180  
ccaacctggt gctgcaacgc accatcgagc ggatacatgt gggcaacgaa tacggcgaca 240  
ttcctcgtgg agtcttcate attcgcggcg agaattgtgt gctactgggc gaaatagtaa 300  
gctttactcg atacattttc aacatgactg attaacaccc tttaaataat cgtaaaaggg 360  
accgtgaaaa ggagcagaaa ctgccactca aagagatatc cgtcgatgaa atcctggacc 420  
cccaacgtag ggaacaggag cagcggcagg agaaacaccg cctagtatcc aagcactaaa 480  
ggacgagcct ggcccgtaga tgccaac 507

&lt;210&gt; 899

&lt;211&gt; 544

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;400&gt; 899

tggtatgtctc ttgccgacgg gaccacctta tggtatttca tcaaaacgct aaaagctgtg 60  
aactggcaac ttataaaaaa aaaggatatt tttttaataa tttgggctac gcctactcta 120  
acgtcaagaa atgtcaaaac ctctagtagga aatacaaact atttcttata catatattgc 180  
atttattcag tcaaacatca gagcgtcgaa gctattattg aaactgtcgc tagatggcgc 240  
acatgtgtca catgtgtctc catctccctt gcactacctt gcaatgacta acgggtatct 300  
gatagtcgaa aagggtgcaa attgaaaaga tgtgcgcaag tatttaataa gctgcgtgaa 360  
atctctgtac agcaattcat tttgggtaat caaataaaaa atataataat ttttcaaaga 420  
tttttaatga cttttaattg acttcaggat gataagagag ttcataaagg caagcaaata 480  
ttctgaattt gaccagagaa ttggtatgta ttataataac gtcattctca tcattaattc 540  
gatt 544

&lt;210&gt; 900

&lt;211&gt; 528

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

585/586

&lt;400&gt; 900

gtgttggcca tatcagagaa cctgtcagaa aagcgaaaag ggggttcgag ccacgaaggt 60  
ggctttcaca cgtcatgggc ataattgaaa attgacagtt tattgccata ggcacgcccc 120  
cttttggcct cctggccttg ttggccatga ttaaaataac aaaagcacgc aaatacacac 180  
acacacacac aactcaacc acacacactc actccggcga tgcttgtcta catcgccgtg 240  
aagacggacg tcttaaatac acgctgcgcg aaatactcga aaccatagta gttgtgtcgg 300  
cccgggtgtg gcggcaatct agcaaaacca cacgggtggga gtcgcgcccc tagttctgcg 360  
ctgcaatcac gccgagttaa ttgtgcgcct gttccgggta aataggtaat ttattatctt 420  
gcgattattg cagcggataa agcagctgat agcgtgcga acttgcgac ggggcgatct 480  
ggaaaggaaa gcgttgcaga caaccgggtg gatcagtggt tgtgttgc 528

&lt;210&gt; 901

&lt;211&gt; 521

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;400&gt; 901

gtttggacat cacaaagtct ccgaaaggct aactttactt tctccacatc gcccaaggcg 60  
aagtagcaga gtaagagggtg aatgctactt ctaatgtttg cccgctccgt catgatgaac 120  
tcaaagctag aagcagcatc tgaataagag cccatgcgaa taaaaaggat tccaatgttt 180  
tcacggatct ttagccttaa ctgacttaag ctctttggta cagaatcaag ggccatgcgg 240  
tacattttta ccgccttttg gtaaataccc atgctgtagt agatgttacc catatttagt 300  
tttagctgat tgacgtgtgg aaacatcttg tttttggcca taatgctgta ggtattgagg 360  
gcttcgatgt gcattctact ccgttcgtat tgctccgcga gattaacaaa aacctatagt 420  
ccatatatat taaagtttta aattatcctt ctaatcgtgc ttaccgcata tgtcaaactg 480  
aaagttgtga taaacatttc accgtgctgg tctcaaattg g 521

&lt;210&gt; 902

&lt;211&gt; 378

586/586

&lt;212&gt; DNA

<213> *Drosophila melanogaster*

&lt;400&gt; 902

ggcgcgtaact aagttaacca ttcggattgc accaatacaa ttgcctcttg aatttcacca 60  
gagcgggggaa ggttcgggaa tataatattg ccatttatgg aagtggatct gcctaattgag 120  
aactgcgttt cccggaaaga ggtgcaccaa tcgaccttaa gtttacaaga tcaccaaagt 180  
tgaaagaatt aattttttta tctaaaaaca aaagtgaaaa ctctcaaaac aataaacaaa 240  
aacggcagtg aaataccact ttcaaacaaa caaaatttat aaaatatttc ttaaagctgt 300  
aaacagtggc gcattcgcaa tgcattttgc caaaaaacaa acgccacaca tggatatgtg 360  
tatggtatgg gaatatgt 378